

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 07:43:47 ; Search time 11596 Seconds

(without alignments)
1145.964 Million cell updates/sec

Title: US-09-719-485-1

Perfect score: 3066
1 ttgaattatctgtcactg.....acgtgaagacgatggataa 3066

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_hng:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
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13: gb_un:*
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15: em_da:*
16: em_fun:*
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20: em_om:*
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33: em_hng_mus:*
34: em_hng_pln:*
35: em_hng_rtd:*
36: em_hng_mam:*
37: em_hng_vrt:*
38: em_sy:*
39: em_hngo_hum:*
40: em_hngo_mus:*
41: em_hngo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	3066	100.0	3066	6	BD211242	BD211242 Cloning a
2	3050.8	99.5	163284	9	AL137000	AL137000 Human DNA
3	3050.8	99.5	341560	2	AL1596304	AL1596304 Homo sapi
4	3050.8	99.5	341580	6	AX711879	AX711879 Sequence
5	3050.8	99.5	341580	6	AX713961	AX713961 Sequence
6	2026	66.1	2040	9	AF034632	AF034632 Homo sapi
7	1038	33.9	1161	6	AX154591	AX154591 Sequence
8	1038	33.9	1161	6	BD211244	BD211244 Cloning a
9	901	29.4	1239	6	AX154589	AX154589 Sequence
10	901	29.4	1239	6	AX549187	AX549187 Sequence
11	901	29.4	1239	6	AX572865	AX572865 Sequence
12	901	29.4	1239	6	BD211243	BD211243 Cloning a
13	900	29.4	1239	6	BD211249	BD211249 Cloning a
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15	591.2	19.3	692	9	HSB342408	AJ342408 Homo sapi
16	576.4	18.8	615	9	HSB339459	AJ339459 Homo sapi
17	550.6	18.0	674	9	HSB330081	AJ330081 Homo sapi
18	487.8	15.9	703	9	HSB340216	AJ340216 Homo sapi
19	480.4	15.7	742	9	HSB340035	AJ340035 Homo sapi
20	478.6	15.6	807	9	HSB337736	AJ337736 Homo sapi
21	444.8	14.5	746	9	HSB341117	AJ341117 Homo sapi
22	443.8	14.5	701	9	HSB326768	AJ326768 Homo sapi
23	414.4	13.5	749	9	HSB323055	AJ323055 Homo sapi
24	411	13.4	693	9	HSB340953	AJ340953 Homo sapi
25	404.4	13.2	722	9	HSB340215	AJ340215 Homo sapi
26	402	13.1	681	9	HSB341310	AJ341310 Homo sapi
27	386	12.6	816	9	HSB340651	AJ340651 Homo sapi
28	338	11.0	602	6	BD211251	BD211251 Cloning a
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33	283	9.2	283	6	AR303910	AR303910 Sequence
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35	283	9.2	283	6	BD064652	BD064652 Human gal
36	283	9.2	283	6	BD064664	BD064664 Mouse gal
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38	250.2	8.2	1703	5	AB095996	AB095996 Gallus ga
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40	250.2	8.2	4121	5	AB095994	AB095994 Gallus ga
41	248.2	8.1	1050	6	AR429668	AR429668 Sequence
42	248.2	8.1	1050	6	BD222611	BD222611 Canine gr
43	234.8	7.7	1063	6	AR156351	AR156351 Sequence
44	234.8	7.7	1101	4	SSU60178	U60178 Sus scrofa
45	233.2	7.6	870	4	SSU60180	U60180 Sus scrofa

ALIGNMENTS

RESULT 1
BD211242
LOCUS BD211242 3066 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211242
VERSION BD211242.1 GI:33021012
KEYWORDS JP 2002517507-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 3066)
Feighner,S.D., Patchett,A.A., Tan,C., McKee,K., Macneil,D.,
Howard,A.D., Peng,S.S. and Smith,R.G.
Cloning and identification of motilin receptor

JOURNAL Patent: JP 2002517507-A 1 18-JUN-2002;
MERCK AND CO INC
COMMENT OS Homo sapiens (human)
PN JP 2002517507-A/1
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PR 12-JUN-1998 US 60/088098
PI SCOTT D FEIGENBER, ARTHUR A PATCHETT, CARINA TAN, KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD, SHENG SHUNG PONG, ROY G SMITH
PC C07K14/705, A61K38/00, A61P1/00, C12N15/09, C1201/02, A61K37/02, PC
C12N15/00
CC Cloning and identification of motilin receptor. FH Key
Location/Qualifiers
FT source 1..3066
Location/Qualifiers
1..3066
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Query Match 100.0%; Score 3066; DB 6; Length 3066;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3066; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TTGAATTATCTGGTCACTGCCGGCGCGGGTGGCTCAAGCTGTATATCCAGACTTTGG 60
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DB 61 GAGGTCAGAGCGGGTGGACCACTGGGGTCAAGAGTTCAGACCAAGCTGGCCAACTGG 120
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DB 301 AGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAATTTATTTGGTCAATTATAT 360
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DB 361 GGTCAAGCTCTCCACCACTCGGAAATTTACAGAAAGAGAGAACTGGGCTGGCGAGACC 420
QY 421 AGGACTAGCCAGATTACAGAAAGTAACTGGTGGAGCCAGAGATTGAGAGAGAGG 480
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QY 661 GCTGTCTAGGGTGACATCGCTCAACGGACCGGGTAGGGCTCTGTGCGCTAAGGCGCC 720
DB 661 GCTGTCTAGGGTGACATCGCTCAACGGACCGGGTAGGGCTCTGTGCGCTAAGGCGCC 720
QY 721 GGGTATTCAGATTAGTGAAGAGGAAAGGAGCCCTGGAAGTGAAGGAGGAGGAGGCG 780
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QY 781 CGGAGCGGAGAGATGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCGG 840
DB 781 CGGAGCGGAGAGATGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGGCGG 840
QY 841 CTAGCTGGAGAGCGGCTGGAGAGCCACCGGAGAGGCGCTTCTGGGCGCGGAGGCGCA 900
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QY 1081 GGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
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DB 1141 TGGTGGCGGAGACGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAGCTGTGAG 1200
QY 1201 TGACCGTGAATCTGATGGGGGCTACCGGAGCATGGAGACACCACTTGTACTGG 1260
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QY 1681 GCGCGTGGGAG 1740
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QY 1741 GCGCGGAG 1800
DB 1741 GCGCGGAG 1800

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 Db 1801 TGCCCTTTCTGTGCTCAGCATCCTCTACGCGGCTCATCGCGCGGAGCTGTGAGAGACC 1860
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 Db 2221 TGGTAATTTCTTAATCCAAACGCTGTAGATGCGACAATGAGGAGTCTTCAAGTCTC 2280
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 Db 2401 ATTCTTTTCAACAGAGAAAGTAAGTCTGTCCGAAGTGGGTTTGGGAAGAGCTTG 2460
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 QY 2521 TATGGAGGCTACTATGAGATTTTAAAGCAAGTATCATGAGCTCAGCGTGTGAT 2580
 Db 2521 TATGGAGGCTACTATGAGATTTTAAAGCAAGTATCATGAGCTCAGCGTGTGAT 2580
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 Db 2701 AATCCCGTGTGTCTTATGTTGAGTGTGTGTTGCGGATTTAATTAATTTGCTG 2760
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 Db 3001 GGGGACACTGAGAGACACGCTGGGCTTACACCGAGACAAAGCGTAAAGAGATG 3060
 QY 3061 GGATTA 3066
 Db 3061 GGATTA 3066

RESULT 2
 AL137000
 LOCUS
 DEFINITION
 Human DNA sequence from clone RP11-203116 on chromosome 13 contains the gene for KIAA0970 protein, COX7C1 (cytochrome c oxidase subunit VIIC pseudogene 1), a novel pseudogene, the GPR38 (G protein-coupled receptor 38) gene, ESTs, STSs, GSSs and a CpG island, complete sequence.
 AL137000
 VERSION
 HTG; COX7C1; CpG island; cytochrome c oxidase; G protein-coupled receptor; GPR38; KIAA0970.
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 163284)
 Wall, M.
 Direct Submission
 Submitted (18-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 JOURNAL
 requests: clonerequest@sanger.ac.uk
 COMMENT
 On Aug 29, 2000 this sequence version replaced gi:9926419.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Bm: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormBase; Information on the WORMBASE database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormbase
 This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr13
 IMPORTANT: This sequence is not the entire insert of clone RP11-203116. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
 The true left end of clone RP11-452110 is at 1 in this sequence. The true right end of clone RP11-103318 is at 163284 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. RP11-203116 is from the library RPI1-11.1 constructed by the group of Pieker de Jong. For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: pBAC3.6.

FEATURES
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 1..163284
 /organism="Homo sapiens"
 /mol_type="genomic DNA"

Query Match	99.5%;	Score 3050.8;	DB 9;	Length 163284;
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Matches 3064;	Conservative	0;	Mismatches 2;	Indels 2;
				Gaps 1;

QY	1	TTGAAATTATTCGTGTA	CTGCGCGGCGCGG	TGGCTCA	GCGCTGTATTC	CAAGAC	CTTTG	60
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QY	61	GAGGTCGAGGCGGGT	GACCA	CTTGGGGTCA	GGAATTG	GAGAC	CGGCTGG	120
Dp	143380	GAGGTCGAGGCGGGT	GACCA	CTTGGGGTCA	GGAATTG	GAGAC	CGGCTGG	143439
QY	121	CGAACCCTGAC	CTACCA	CAAAAAAC	CAAAATT	TACCGGGGCTT	GGCGCTCTG	180
Dp	143440	CGAACCCTGAC	CTACCA	CAAAAAAC	CAAAATT	TACCGGGGCTT	GGCGCTCTG	143499
QY	181	CCAGTACT	CAAGAGGCT	GAGTGGAG	ACTGT	TGAGCT	TGGAGGTCGAG	240
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QY	241	TGAGCTGTAT	CGCGCCACT	TAAAT	CTCCAGCT	TGAGCA	CAAGTGAACCT	300
Dp	143560	TGAGCTGTAT	CGCGCCACT	TAAAT	CTCCAGCT	TGAGCA	CAAGTGAACCT	143619
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Dp	143680	GGTCAGCT	CCCTC	CACCACT	CGCGAATTA	CAAGAGAG	AGAACTGGGCTGG	143739
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Dp	143800	CTTAGATT	TCTGGTCT	TAAGT	CTCCCTCCT	TATTA	TAGATTAG	143859
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Dp	143860	CCATAGAC	CCCTCT	CTCACCGT	CAAGGGGAG	CTAC	CAACCA	143919
QY	601	AGGTGCC	CGGAGTA	CCAGACT	GA	CAAAAG	CGCTCT	660
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QY	661	GCTGTCT	AGGTCAC	ACATTCG	CTCACCGG	AGCTG	CTGTA	720
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Dp	144040	GGGATATT	CCAGTTA	GTGTGA	AGGAAAG	CGCTCT	GA	144099
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Dp	144100	CGGAGAG	CGACAT	TGCGCGG	CGGGGCGG	CGCGGCT	GTG	144159
QY	841	CTAGCT	CGGAGCG	CTCGAG	CCCA	CCCGCA	AGCGCTT	900
Dp	144160	CTAGCT	CGGAGCG	CTCGAG	CCCA	CCCGCA	AGCGCTT	144219
QY	901	GGCGAG	CGCTCG	CGCTGA	CCCTG	CGCGG	CGCGGCT	960
Dp	144220	GGCGAG	CGCTCG	CGCTGA	CCCTG	CGCGG	CGCGGCT	144279
QY	961	CTCA	CCGAGG	GA	CCAC	CGCGGCT	CTCA	1020
Dp	144280	CTCA	CCGAGG	GA	CCAC	CGCGGCT	CTCA	144339

QY	1201	GAGACACCAATGGAGAGCCCTGGAAAGGACAGCAGCGCCCCAGAGGGAGGAGCGAGAGCCGC	1080
Db	144340	GAGACACCAATGGAGAGCCCTGGAAAGGACAGCAGCGCCCCAGAGGGAGGAGCGAGAGCCGC	144359
QY	1081	CGTAGGCCCGAGCTGCGCCTTGGCAGAGAGCGCGCTGTCGCGCTTTCCTGGAGCGCG	1140
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 REFERENCE
 1 Zhang, Y., Mofkelt, M., Cookson, W. and Tinsley, J. O.
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AX739961

LOCUS AX739961 34980 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 1 from Patent WO0300296.

ACCESSION AX739961

VERSION AX739961.1 GI:30519236

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Zhang, Y., Moffatt, M. and Cookson, W.

TITLE Treatment and diagnosis of B cell chronic lymphocytic leukaemia

JOURNAL Patent: WO 0300296-A 1 03-JAN-2003;

ISIS INNOVATION LIMITED (GB)

FEATURES

source

1. .34980

Location/Qualifiers

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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;

Matches 3064; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

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Db 37048 GAGGTGAGCGCGGTGAGCACTCTGGGCTCAGAGCTTCAGACCAAGCTGGCAACATGG 37107

QY 121 CGAAACCTGACTACACAAAAACAAATTTAGCCGGGCTTGGGCGCTCTGTGCTC 180

Db 37108 CGAAACCTGACTACACAAAAACAAATTTAGCCGGGCTTGGGCGCTCTGTGCTC 37167

QY 181 CCGACTACTGAGAGGCTGAGTGGAGAGCTGTTGAGCTTGGAGGTTCAGAGCTGAG 240

Db 37168 CCGACTACTGAGAGGCTGAGTGGAGAGCTGTTGAGCTTGGAGGTTCAGAGCTGAG 37227

QY 241 TGAAGTGTGATGCGCGCACTTAACTCCAGCTGAGACAGTGAAGACCTGTCTCAAGA 300

Db 37228 TGAAGTGTGATGCGCGCACTTAACTCCAGCTGAGACAGTGAAGACCTGTCTCAAGA 37287

QY 301 AGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAATTTTGGTCAATTATAT 360

Db 37288 AGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAATTTTGGTCAATTATAT 37347

QY 361 GGTGACGCTCCCTCCACCACTCGGCAATTACAGAAAGAGAGCACTGGGCTGGGCGAGACC 420

Db 37348 GGTGACGCTCCCTCCACCACTCGGCAATTACAGAAAGAGAGCACTGGGCTGGGCGAGACC 37407

QY 421 AGGACTAGGCCAAGATTACAAAGTTACTCGGTTGTAGAGCCAGAGATTAGACAGAGAGG 480

Db 37408 AGGACTAGGCCAAGATTACAAAGTTACTCGGTTGTAGAGCCAGAGATTAGACAGAGAGG 37467

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LOCUS	AF034632		2040 bp DNA linear	AF034632			Homo sapiens (human)								
DEFINITION	Homo sapiens orphan G protein-coupled receptor (GPR38) gene,						Homo sapiens (human)								
ACCESSION	AF034632						Homo sapiens (human)								
VERSION	AF034632.1						Homo sapiens (human)								
KEYWORDS	GI:2654158						Homo sapiens (human)								
SOURCE							Homo sapiens (human)								
ORGANISM							Homo sapiens (human)								
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RESULT 7
LOCUS AX154591 1161 bp DNA linear PAT 23-JUN-2001
DEFINITION Sequence 11 from Patent WO0138355.
ACCESSION AX154591
VERSION AX154591.1 GI:14536177
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Shepard,P.O., Jaspers,S.R., Deisher,T.A. and Bishop,P.D.
TITLE Method of forming a peptide-receptor complex with zsig3 and
therapeutic use thereof
JOURNAL Patent: WO 0138355-A 11 31-MAY-2001;
Zymogenetics, Inc. (US)
FEATURES
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Query Match 33.9%; Score 1038; DB 6; Length 1161;
Best Local Similarity 99.8%; Pred. No. 4.4e-153;
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1029 ATGGGCAAGCCCTTGGAACGGACGAGCGCCCGAGGGGGCGGGAGACCGCCGTGGCC 1088
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QY 1089 GCGGTGGCGCTTGGCCAGCGAGCGCGCGTGTCCGCTTTCCCTGGGGGGCGGTGGCGG 1148
DB 61 GCGGTGGCGCTTGGCCAGCGAGCGCGCGTGTCCGCTTTCCCTGGGGGGCGGTGGCGG 120
QY 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1208
DB 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 180
QY 1209 ATGCTGATGCGGGGCTACCGGGACATCGGACCAACCACTTGTACTGTGGGACGATG 1268
DB 181 ATGCTGATGCGGGGCTACCGGGACATCGGACCAACCACTTGTACTGTGGGACGATG 240
QY 1269 GCGGTGGCCAGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1328
DB 241 GCGGTGGCCAGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 1329 TCGGGGCGCTTGGGTGTGGGCGCGCTGTGCGCGCTGTGCTGTACTGTTGGGCGAGGCG 1388
DB 301 TCGGGGCGCTTGGGTGTGGGCGCGCTGTGCGCGCTGTGCTGTACTGTTGGGCGAGGCG 360
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DB 421 TGCGGCGCGCTTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGT 480
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QY 1569 CAGAACCGCGGACATCTCCGTAGTCCCGGCGCTCAATGACACCGGCGGATGCGCTCCG 1628
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LOCUS BD211244 1390 bp DNA linear PAT 17-JUL-2003
DEFINITION Cloning and identification of motilin receptor.
ACCESSION BD211244
VERSION BD211244.1 GI:33021014
KEYWORDS JP 2002517507-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Feighner,S.D., Patchett,A.A., Tan,C., McKee,K., Macneil,D.,
Howard,A.D., Pong,S.S. and Smith,R.G.
TITLE Cloning and identification of motilin receptor
JOURNAL Patent: JP 2002517507-A 3 18-JUN-2002;
MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002517507-A/3
PD 18-JUN-2002
PF 08-JUN-1999 JP 2000553444
PI 12-JUN-1998 US 60/089098
PI SCOTT D FEIGNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE, PI
DOUGLAS MACNEIL,
PI ANDREW D HOWARD,SHENG SHUNG PONG ROY G SMITH
PC 027K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC
C12N15/00
CC Cloning and identification of motilin receptor. FH Key
Location/Qualifiers 1..1390
FT source

FEATURES FT
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Query Match 33.9%; Score 1038; DB 6; Length 1390;
 Best Local Similarity 99.8%; Pred. No. 4.4e-153;
 Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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 Best Local Similarity 99.8%; Pred. No. 4.4e-153;
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 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208
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 1869 CTGCGAGGCGCGCGCTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1928
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Db 901 CGTAAGTGAAGCGCGCTGTCTCAAAAGACGCTGTGCTGCACTGTGCGCGCGCGCGGAGAC 960
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RESULT 9
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 LOCUS
 DEFINITION Sequence 9 from Patent WO0138355.
 ACCESSION AX154589
 VERSION AX154589.1 GI:14536175
 KEYWORDS
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 METHOD OF FORMING A PEPTIDE-RECEPTOR COMPLEX WITH ZS193 AND
 THERAPEUTIC USE THEREOF
 PATENT: WO 0138355-A 9 31-MAY-2001;
 ZymoGenetics, Inc. (US)
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 VMAVALISAGPLFLVGVEDPDGIVSVGLNGTARIASPLASPPMLSRAPSP
 RSGPRTAAALPSRRCRSPALDGLRVMVTVAYPAFLICSLIYGLIGRLMS
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ORIGIN
 Query Match 29.4%; Score 901; DB 6; Length 1239;
 Best Local Similarity 100.0%; Pred. No. 1.3e-131;
 Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 1089 GCGCTGCGCGCTTGGACGAGCGCGCGCTGCGCCCTTCCCTGGGAGCGCTGGTGGCG 1148
 61 GCGCTGCGCGCTTGGACGAGCGCGCGCTGCGCCCTTCCCTGGGAGCGCTGGTGGCG 120
 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208
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QY 1329 TCGGAGCCCTGGGTTTCGGGCGGCTGCTGCGCCCTGTCCCTTACGTGGGCGAGGCG 1388
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QY 1689 GGGCCCGAGACCGGCGGAGCGCGGCGCTGTTACAGCCCGGATGCGGCGAGCCCGCG 1748
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QY 1749 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACACCGCTTACTTTCTTCCCTTT 1808
DB 721 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACACCGCTTACTTTCTTCCCTTT 780
QY 1809 CTGTGCTCAAGCATCTCTACGGGCTCATGCGGCGGAGCTGTGAGACACCGGCGGCG 1868
DB 781 CTGTGCTCAAGCATCTCTACGGGCTCATGCGGCGGAGCTGTGAGACACCGGCGGCG 840
QY 1869 CTGCGAGGCGCGCGCGCTCTGCGGCGGAGAGAGCCACCGGCGAGACCGTCCGCTCTG 1928
DB 841 CTGCGAGGCGCGCGCGCTCTGCGGCGGAGAGAGAGCCACCGGCGAGACCGTCCGCTCTG 900
QY 1929 C 1929
DB 901 C 901

RESULT 10
AX549187 1239 bp DNA linear PAT 26-NOV-2002
LOCUS AX549187
DEFINITION Sequence 472 from Patent WO02061087.
ACCESSION AX549187
VERSION AX549187.1 GI:25813904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 472 08-AUG-2002;
JOURNAL Lifespan Biosciences, Inc. (US)
FEATURES
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Best local Similarity 100.0%; Pred. No. 1.3e-131;

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QY 1089 GCGCTGCGGCTTGGAGAGAGCGCGGCTGCGGCTTCCCTTGGGCGCGCTGCGG 1148
DB 61 GCGCTGCGGCTTGGAGAGAGCGCGGCTGCGGCTTCCCTTGGGCGCGCTGCGG 120
QY 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208
DB 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
QY 1209 ATGCTGATCGGCGGCTTACCGGAGCATGAGGACACACACACTTGTACTTGGGAGCATG 1268
DB 181 ATGCTGATCGGCGGCTTACCGGAGCATGAGGACACACACACTTGTACTTGGGAGCATG 240
QY 1269 GCGGCTGCGACTTACTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 1328
DB 241 GCGGCTGCGACTTACTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 300
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DB 301 TCGCGGCGCTGAGTGTTCGCGCGGCTGTGCGGCTGTGCGGCTGTGCGGCTGTGCG 360
QY 1389 TGCACCTACGCGACGCTGTGACATATGACCGGCGGCTCATATGACCGGCGGATCCGCTCTCG 1448
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QY 1449 TGCAGCCCTGCTCCGCGCCGCGCTTGTGTACACCGGCGCGGCTCCGCGCTCATGCT 1508
DB 421 TGCAGCCCTGCTCCGCGCCGCGCTTGTGTACACCGGCGCGGCTCCGCGCTCATGCT 480
QY 1509 GTGCTCTGGGCGCGTGGGCGGCTCTGCGGCTCCCTTCTTGTCTGAGTGGGCGTCCAG 1568
DB 481 GTGCTCTGGGCGCGTGGGCGGCTCTGCGGCTCCCTTCTTGTCTGAGTGGGCGTCCAG 540
QY 1569 CAGGACCCCGGCACTTCCTGATGCCGAGGCTCATATGACACCGGCGGATCCGCTCTCG 1628
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QY 1749 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACACCGCTTACTTTCTTCCCTTT 1808
DB 721 CAGCTGGGCGCGCTGCTGTGATGCTGTGGGTACACACCGCTTACTTTCTTCCCTTT 780
QY 1809 CTGTGCTCAAGCATCTCTACGGGCTCATGCGGCGGAGCTGTGAGACACCGGCGGCG 1868
DB 781 CTGTGCTCAAGCATCTCTACGGGCTCATGCGGCGGAGCTGTGAGACACCGGCGGCG 840
QY 1869 CTGCGAGGCGCGCGCGCTCTGCGGCGGAGAGAGCCACCGGCGAGACCGTCCGCTCTG 1928
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QY 1929 C 1929
DB 901 C 901

RESULT 11
AX572965 1239 bp DNA linear PAT 29-NOV-2002
LOCUS AX572965
DEFINITION Sequence 1 from Patent WO02057791.
ACCESSION AX572965
VERSION AX572965.1 GI:26005013

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QY	1869	CTGGGAGGCGCGGCGCGCTTCGGGGCGGGAGAGAGCCACCGGACGCGTCCGCTCTG	1928
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QY	1929	C 1929	
Db	901	C 901	
RESULT 12			
LOCUS	BD211243	1239 bp	DNA linear PAT 17-JUN-2003
DEFINITION	Cloning and identification of motilin receptor.		
ACCESSION	BD211243		
VERSION	BD211243.1		
KEYWORDS	JP 2002517507-A/2.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (Bases 1 to 1239)		
AUTHORS	Feighner,S.D., Patchett,A.A., Tan,C., Mckee,K., Macneil,D., Howard,A.D., Pong,S.S. and Smith,R.G.		
TITLE	Cloning and identification of motilin receptor		
JOURNAL	Patent: JP 2002517507-A 2 18-JUN-2002; MERCK AND CO INC		
COMMENT	OS Homo sapiens (human) PN JP 2002517507-A/2 PD 18-JUN-2002 PF 08-JUN-1999 JP 2000553444 PR 12-JUN-1998 US 60/089098 PI SCOTT D FEIGHNER,ARTHUR A PATCHETT,CARINA TAN,XAREN MCKEE, PI DOUGLAS MACNEIL, PI ANDREW D HOWARD,SHENG SHUNG PONG,ROY G SMITH PC C07314/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC C12N15/00 CC Cloning and identification of motilin receptor. FH Key CCT Cloning and identification of motilin receptor. FH Key FT source 1. 1239 FT Location/Qualifiers 1. 1239 /organism='Homo sapiens (human)'. Location/Qualifiers 1. 1239 /organism='Homo sapiens' /mol_type='genomic DNA' /db_xref='taxon:9606'		
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ORIGIN			
Query Match	29.4%; Score 901; DB 6; Length 1239;		
Best Local Similarity	100.0%; Pred. No. 1,3e-131;		
Matches	901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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QY	1089	GCGGTGCGGCTTGGCGAGAGCGCGGTGTCGCGCTTCCCTGGGGGGCGCTGTGTCG	1148
Db	61	GCGGTGCGGCTTGGCGAGAGCGCGGTGTCGCGCTTCCCTGGGGGGCGCTGTGTCG	120
QY	1149	GTCAGCGCTGTGTGCTCTGTGCTTTGTCGTGCGGGGTGAGCGGCAAGTGTGACCGTG	1208
Db	121	GTCAGCGCTGTGTGCTCTGTGCTTTGTCGTGCGGGGTGAGCGGCAAGTGTGACCGTG	180
QY	1209	ATGCTGATGGGGGGGCTATCGGGGACATCGGAGACACCAACCAATTGTACTCTGGGAGAGATG	1268
Db	181	ATGCTGATGGGGGGGCTATCGGGGACATCGGAGACACCAACCAATTGTACTCTGGGAGAGATG	240
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Db 781 CTGAGCTTACGCACTCTCTACGCGGCTCATGCGGCGGAGCTGTGAGACGACCGCGCGCG 840
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Db 901 C 901

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PC C07K14/705,A61K38/00,A61P1/00,C12N15/09,C12Q1/02,A61K37/02, PC
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FT source 1..900
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/location/Qualifiers
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Query Match 29.4%; Score 900; DB 6; Length 900;
Best Local Similarity 100.0%; Pred. No. 1.9e-131;
Matches 900; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION BD211249
 ACCESSION BD211249.1 GI:33021019
 VERSION JP 2002517507-A/8.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Feighner,S.D., Patchett,A.A., Tan,C., McKee,K., Macneil,D.,
 Howard,A.D., Pong,S.S. and Smith,R.G.
 Cloning and identification of mollin receptor
 Patent: JP 2002517507-A 8 18-JUN-2002;
 MERCK AND CO INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002517507-A/8
 PD 18-JUN-2002
 PF 08-JUN-1999 JP 200053444
 PR 12-JUN-1998 US 60/089098
 PI SCOTT D FEIGNER,ARTHUR A PATCHETT,CARINA TAN,KAREN MCKEE, PI
 DOUGLAS MACNEIL,
 PI ANDREW D HOWARD,SHENG SHUNG PONG,ROY G SMITH

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VERSION	AJ339407.1	GI:15883825	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 692)		
AUTHORS	Kurenkov, A.S., Gizaullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podolski, R.M., Matushkin, Y.G., Granchandani, A., Muravenko, O.V., Levitskiy, V.G., Kolchanov, N.A., Protodopov, A.I., Kashba, V.I., Kiselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.		
TITLE	NotI flanking sequences: a tool for gene discovery and verification of the human genome		
JOURNAL	Nucleic Acids Res.	30 (14), 3163-3170	(2002)
MEDLINE	22131767		
PUBMED	12136098		
REFERENCE	2 (bases 1 to 692)		
AUTHORS	Zabarovsky, E.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-MAY-2001) Microbiology and Tumoriology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden		
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Db	121	CGTGGGGGCGGTGGTGCACCGGACCGCGTGTGTGCTGTGCTGTTCGTCGTCGGGGGTGAG	180
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Db	181	CGGCAACGTGTGACCGTGTGATGTGATGGGCGGTACCGGACATGGGACCAACACCAA	240
QY	1250	CTGTGTACCTGGGGACGATGGCGCGTGTCCGACCTTACCTGCTGGGGTCCGCTTTCGA	1309
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QY	1310	CGTGTACCGCTCTGAGGCGTTCGCGAGCCCTTGAGTGTGGGCGCGCTGCTTCGCGCTGTC	1369
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ORGANISM	Homo sapiens		
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OY	1070	GGGCGAGCGCGCGTGGCG	1129
Db	61	GGGCGAGCGCGCGTGGCG	120
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QY 1190 CGGCAAGCTGGTGAACCGTATGATCGGCGCTACCGGAGCATGCGGACCAACCA 1249
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XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;
PI Pong S, Smith RG;
XX WPI; 2000-105868/09.
XX Novel receptor protein for screening compounds used in treating irritable
PT bowel syndrome, constipation and other gastric conditions.
XX
PS Example 1; Fig 1; 44p; English.

XX
XX The present sequence represents the genomic sequence of the motilin
CC receptor gene, including the 5' untranslated region (5' UTR). This gene
CC encodes a G-protein coupled receptor, and is designated MTL-R1 (also
CC GPR38). Two spliced forms of GPR38 exist, MTL-R1A (see A454145) and MTL-
CC R1B (see A454146). MTL-R1A is a functional seven transmembrane domain
CC form, and MTL-R1B is a truncated five transmembrane domain
CC protein. Both are used to identify agonists and antagonists which can be used
CC for treating gastric motility disorders, functional defects, disorders
CC secondary to neurological disorders e.g. scleroderma, paraneoplastic
CC syndromes radiation induced dysmotility, diabetes, infections, stress-
CC related motility disorders, psychogenic disorders, gastroparesis, gastro-
CC oesophageal reflux disease, constipation, chronic idiopathic pseudo
CC obstruction, acute faecal impaction, postoperative ileus, gallstones,
CC infantile colic, irritable bowel syndrome, non-ulcer dyspepsia, non-
CC cardiac chest pain and diarrhoea. They can also be used in the
CC preparation for colonoscopy, endoscopy and duodenal intubation
XX

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Best Local Similarity 100.0%; Pred. No. 0;
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 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 294727..309803
 FT /*tag= a "CLND8"
 FT /product= "CLND8"
 FT /*tag= b
 FT /product= "NY-REN-34"
 XX
 PN MO2003000296-A2.
 XX
 PD 03-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-GB002857.
 XX
 PR 21-JUN-2001; 2001GB-00015211.
 XX
 PA (ISIS-) ISIS INNOVATIONS LTD.
 XX
 PI Zhang Y, Mofatt M, Cookson W;
 XX
 DR WPI; 2003-221370/21.
 XX
 PT Treating B-cell chronic lymphocytic leukemia in an individual by
 PT modulating the expression of the CLND8 and/or the NY-REN-34 gene.
 XX
 PS Disclosure; Fig 1; 154bp; English.
 XX

Db 37828 CTAGCTCGGAGCGCCTCGGAGCCCACCCCGAGAGCCGCTTCTCGCGCCCCCGCAGCGCA 37887

[illegible]

Db 38968 CGGGAGCCGGCAAGCTGGGTCCTCCCTCCCTGCTCGCCGAGCTCTGGGCGCGCTTC 39027
QY 2041 CAGCTCCC--TCTATTTCGATTCAGCTCCACCCGCGGATCTCCCATCCCCGAGA 2098
Db 39028 CAGCTCCCTTTCCTATTTCATTCAGCCCTCCACCCGCGGATCTCCCATCCCCGAGA 39087
QY 2099 AAACCATGTCTGTCCCGCCGAGAGCTCTGGGGAGACCCGAGCGCTTTGAGGGTGGGATC 2158
Db 39088 AAACCATGTCTGTCCCGCCGAGAGCTCTGGGGAGACCCGAGCGCTTTGAGGGTGGGATC 39147
QY 2159 CCGGATCCGATTCAGTACACAGCAGTGTCTTTTCAGAGCTCTGAGACCAAGAGAGA 2218
Db 39148 CCGGATCCGATTCAGTACACAGCAGTGTCTTTTCAGAGCTCTGAGACCAAGAGAGA 39207
QY 2219 GTTGGTATCTCTTAATCCACACCTGTTAGTCCCAATGAGAGTCTCACAGTGC 2278
Db 39208 GTTGGTATCTCTTAATCCACACCTGTTAGTCCCAATGAGAGTCTCACAGTGC 39267
QY 2279 TCTTGAGAGACGAGGAGATTCATTAGCTAAATTTTATTATTATTATTATTATTATTATT 2338
Db 39268 TCTTGAGAGACGAGGAGATTCATTAGCTAAATTTTATTATTATTATTATTATTATTATT 39327
QY 2339 CTGAGGCTTAAGTAACTTTGCTCTGATCAAAAAGTAAAGATTGGCAGACCTGTGTA 2398
Db 39328 CTGAGGCTTAAGTAACTTTGCTCTGATCAAAAAGTAAAGATTGGCAGACCTGTGTA 39387
QY 2399 GAATCTTTTCAACAGAGAACAGAAAACCTTGCTCCGAGTGGTGTGTGGAAGAGAGCC 2458
Db 39388 GAATCTTTTCAACAGAGAACAGAAAACCTTGCTCCGAGTGGTGTGTGGAAGAGAGCC 39447
QY 2459 TGCCAGCGCGCTTGTTCAGAGAAATTGCTCTCTGTTATGTCCAGCTTGATPACA 2518
Db 39448 TGCCAGCGCGCTTGTTCAGAGAAATTGCTCTCTGTTATGTCCAGCTTGATPACA 39507
QY 2519 CATATGGAGGCTACTATGATGATTTTAAAGCAATGATGATGAGCTGAGCTGTGTA 2578
Db 39508 CATATGGAGGCTACTATGATGATTTTAAAGCAATGATGATGAGCTGAGCTGTGTA 39567
QY 2579 TTTTTCCTGGGGTGAAGATCTGCTAGGTAGAGATTTTCTTAATTTTGTCTTTAC 2638
Db 39568 TTTTTCCTGGGGTGAAGATCTGCTAGGTAGAGATTTTCTTAATTTTGTCTTTAC 39627
QY 2639 TTGTTATTGCAAGATGTTCTTGTTCGCGGGTGGGGGTTATTGCTCCCAATGCTTTG 2698
Db 39628 TTGTTATTGCAAGATGTTCTTGTTCGCGGGTGGGGGTTATTGCTCCCAATGCTTTG 39687
QY 2699 TTAATCCCGAGTGTGTCTTATGTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2758
Db 39688 TTAATCCCGAGTGTGTCTTATGTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 39747
QY 2759 GGTTCCTCTTCCAGTGTGCGAATCATTTTACATTAACCGAAGATTCGGGATGATGT 2818
Db 39748 GGTTCCTCTTCCAGTGTGCGAATCATTTTACATTAACCGAAGATTCGGGATGATGT 39807
QY 2819 ACTTCTCAGTACTTTTAACATCGTGTCTGCACTTTTCTATGTAGCCATCTATCA 2878
Db 39808 ACTTCTCAGTACTTTTAACATCGTGTCTGCACTTTTCTATGTAGCCATCTATCA 39867
QY 2879 ACCCAATCTCTTACAACTCATTTTAAAGAGTACAGAGCGCGGCTTTAACTGCTGC 2938
Db 39868 ACCCAATCTCTTACAACTCATTTTAAAGAGTACAGAGCGCGGCTTTAACTGCTGC 39927
QY 2939 TCGCAAGGAGTCCGAGCGGAGGCTTCCAGAGAGAGGAGACTCGGCGGAGAGTTG 2998
Db 39928 TCGCAAGGAGTCCGAGCGGAGGCTTCCAGAGAGAGGAGACTCGGCGGAGAGTTG 39987
QY 2999 CAGGGAGCACTGAGAGAGACACGCTGGGCTTACACCGAGCAAGCCCTTAACTGAAAGCA 3058
Db 39988 CAGGGAGCACTGAGAGAGACACGCTGGGCTTACACCGAGCAAGCCCTTAACTGAAAGCA 40047
QY 3059 TGGGATTA 3066
|||||

Db 40048 TGGGATTA 40055
RESULT 3
ID AAA46116
AAA46116 standard; cDNA: 2040 BP.
XX AAA46116;
AC 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hGPR38 (V297K) cDNA SEQ ID NO:129.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW Identification; agonist; screening; therapeutic; pharmaceutical; mutant;
KW ss.
OS Homo sapiens.
XX Synthetic.
XX WO200022131-A2.
XX
XX 20-APR-2000.
XX
XX 13-OCT-1999; 99WO-US024065.
XX
XX 13-OCT-1998; 98US-00170496.
XX 12-NOV-1998; 98US-0108022P.
XX 20-NOV-1998; 98US-0109213P.
XX 27-NOV-1998; 98US-0110060P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123944P.
XX 12-MAR-1999; 99US-0123945P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123948P.
XX 12-MAR-1999; 99US-0123949P.
XX 12-MAR-1999; 99US-0123951P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 28-MAY-1999; 99US-0137567P.
XX 29-JUN-1999; 99US-0141448P.
XX 27-AUG-1999; 99US-0151114P.
XX 03-SEP-1999; 99US-0152524P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156533P.
XX 29-SEP-1999; 99US-0156534P.
XX 29-SEP-1999; 99US-0156653P.
XX 01-OCT-1999; 99US-0157280P.
XX 01-OCT-1999; 99US-0157281P.
XX 01-OCT-1999; 99US-0157282P.
XX 01-OCT-1999; 99US-0157293P.
XX 01-OCT-1999; 99US-0157294P.
XX 12-OCT-1999; 99US-00416760.
XX 12-OCT-1999; 99US-00417044.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Brinema K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
XX WPI; 2000-317986/27.
XX P-PSDB; AAB02854.
XX
XX Non-endogenous, human G protein-coupled receptors for screening receptor,
XX Inverse or partial agonists useful as therapeutic agents.
XX Example 2; Page 166-168; 187pp; English.
XX
XX The present invention describes transmembrane receptors, preferably human

Db	1141	GGCCACCGGAGACCGTCCCGCTCCG	1168
RESULT 5			
AAAF83684			
ID	AAAF83684	standard; DNA; 1161 BP.	
XX			
AC	AAAF83684;		
DT	23-JUN-2001	(first entry)	
XX			
DE	Short form of mol11n receptor, GPR-38B isoform encoding DNA.		
XX			
KM	zs1933; signal transduction; hormone; enzymes; neural development;		
KM	gastroic contractility; nutrient uptake; digestive; pancreatic; human;		
KM	insulin-like growth factor-1; growth hormone; bone; gastrointestinal;		
KM	glucose; osteoporotic; anorectic; vulnerability; immunomodulator; GHS-R; ds;		
XX	G-protein coupled receptor; mol11n receptor; GPR38; GPR-38B; isoform.		
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..1161	
FT		/*tag= a	
FT		/product= "GPR-38B"	
XX			
PN	MO200138355-A2.		
XX			
PD	31-MAY-2001.		
XX			
PF	22-NOV-2000; 2000MO-US032074.		
XX			
PR	22-NOV-1999; 99US-0166765P.		
XX			
PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Sheppard PO, Taspers SR, Deisher TA, Bishop PD;		
XX			
DR	WPI; 2001-355879/37.		
XX			
DR	P-PSDB; AAB62653.		
XX			
PT	Forming reversible peptide receptor complex for purifying cell and		
PT	peptides, stimulating signal transduction and modulating hormone		
PT	secretion. Involves contacting a receptor with zs1933 polypeptide.		
XX			
PS	Dislosure; Page 106-109; 11np; English.		
XX			
XX			
CC	The invention relates to a method of forming a reversible peptide-		
CC	receptor complex that involves providing an immobilized receptor, and		
CC	contacting the receptor with a zs1933 peptide (comprising residues 24-37		
CC	of AAB62649), where the receptor binds to the zs1933 peptide. The method		
CC	is useful for purifying cells, purifying a peptide, stimulating signal		
CC	transduction in a cell expressing a receptor. It is also useful for		
CC	modulating secretion of hormones, neural development and/or utilization,		
CC	gastroic contractility, nutrient uptake, secretion of digestive and		
CC	pancreatic enzymes and hormones, secretion of insulin-like growth factor		
CC	-1, secretion of non-zs1933 proteins. It is useful for modulating growth		
CC	hormone secretion in a mammal having a disease associated with abnormal		
CC	levels of growth hormone, such as osteoporosis, bone repair, bone		
CC	remodeling, low osteoblast levels, cartilage repair and remodeling,		
CC	skeletal dysplasia, immune suppression, obesity, growth retardation,		
CC	protein catabolic responses after surgery, cachexia, protein loss,		
CC	dwarfism, wound healing and ovulation induction, treating a mammal having		
CC	a metabolic disorder requiring neurological feedback, such as satiety		
CC	regulation, glucose absorption and metabolism and neuropathy-associated		
CC	gastrointestinal disorders, and stimulating glucose-induced insulin		
CC	release in a mammal. The present sequence represents the DNA encoding the		
CC	short form of mol11n receptor, GPR-38B (one of the two isoforms of GPR38		
CC	which result from alternative splicing). GPR38 has homology to the human		
CC	G-protein coupled receptor, GHS-R		
XX			
XX	Sequence 1161 BP; 126 A; 436 C; 372 G; 227 T; 0 U; 0 Other;		

[illegible]

QY 2049 --TCTATTTCGATTCGACCTCCACCCGCG 2078
|||||
Db 1021 TTTCCTATTTCGATTCGACCTCCACCCGCG 1052

RESULT 6

AAZ45404
AAZ45404 standard; cDNA; 1390 BP.

AC AAZ45404;

DT 27-MAR-2000 (first entry)

DE cDNA encoding the motilin receptor splice variant MTL-R1B.

XX Motilin receptor; G-protein coupled receptor; MTL-R1; GPR38;
KM spliced form; MTL-R1A; MTL-R1B; gastric motility disorder;
KM functional defect; neurological disorder; scleroderma; colonoscopy;
KM paraneoplastic syndrome; radiation induced dysmotility; diabetes;
KM infection; stress-related motility disorder; psychogenic disorder;
KM gastroparesis; gastro-oesophageal reflux disease; constipation;
KM chronic idiopathic pseudo obstruction; acute faecal impaction;
KM postoperative ileus; gallstones; infantile colic; diarrhoea;
KM irritable bowel syndrome; non-ulcer dyspepsia; non-cardiac chest pain;
KM endoscopy; duodenal intubation; ds.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 1. .1161
FT CDS /*tag= a
FT /product= "MTL-R1B"

XX MO9964436-A1.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012773.

XX 12-JUN-1998; 98US-0089098P.

XX (MERI) MERCK & CO INC.

XX Feighner SD, Patchett AA, Tan C, McKee K, Macneil D, Howard AD;
PI Pong S, Smith RG;

XX WPI: 2000-105868/09.
DR P-PSDB; AAY54146.

XX Novel receptor protein for screening compounds used in treating irritable
PT bowel syndrome, constipation and other gastric conditions.

XX Claim 6; Fig 4; 44pp; English.

XX The present sequence encodes splice variant MTL-R1B of the motilin
CC receptor. The gene encodes a G-protein coupled receptor, and is
CC designated MTL-R1 (also GPR38). Two spliced forms of GPR38 exist, MTL-R1A
CC (see AAY54145) and MTL-R1B (see AAY54146). MTL-R1A is a functional seven
CC transmembrane domain form, and MTL-R1B is a truncated five transmembrane
CC domain. The MTL-R1 proteins are used to identify agonists and antagonists
CC which can be used for treating gastric motility disorders, functional
CC defects, disorders secondary to neurological disorders e.g. scleroderma,
CC paraneoplastic syndromes radiation induced dysmotility, diabetes,
CC infections, stress-related motility disorders, psychogenic disorders,
CC gastroparesis, gastro-oesophageal reflux disease, constipation, chronic
CC idiopathic pseudo obstruction, acute faecal impaction, postoperative
CC ileus, gallstones, infantile colic, irritable bowel syndrome, non-ulcer
CC dyspepsia, non-cardiac chest pain and diarrhoea. They can also be used
CC in the preparation for colonoscopy, endoscopy and duodenal intubation
XX Sequence 1390 BP; 190 A; 496 C; 436 G; 268 T; 0 U; 0 Other;

Best Local Similarity 99.8%; Pred. No. 3.5e-163;
Matches 1050; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1029 ATGGGACACCCCTGGAAACGACGACGACCGCCCGAGGAGCGGAGCCGCTGGGCC 1088
|||||
Db 1 ATGGGACACCCCTGGAAACGACGACGACCGCCCGAGGAGCGGAGCCGCTGGGCC 60
QY 1089 GGGCTGCCGCTTGGGACGAGCGCGCTGCTGCCCTTTCCCTTGGGGGCGCTGTGCCG 1148
|||||
Db 61 GGGCTGCCGCTTGGGACGAGCGCGCTGCTGCCCTTTCCCTTGGGGGCGCTGTGCCG 120
QY 1149 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1208
|||||
Db 121 GTGACCGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 180
QY 1209 ATGCTGATCGGCGCTACCGGAGACATGCGAGCAACACCAATTGTACCTTGGGACATG 1268
|||||
Db 181 ATGCTGATCGGCGCTACCGGAGACATGCGAGCAACACCAATTGTACCTTGGGAGCATG 240
QY 1269 GCGGCTGCCGCTTGGGACGAGCGCGCTGCTGCCGCTTGGGACGAGCGCTTGGGCGC 1328
|||||
Db 241 GCGGCTGCCGCTTGGGACGAGCGCGCTGCTGCCGCTTGGGACGAGCGCTTGGGCGC 300
QY 1329 TCGCGGCGCTTGGGAGCGCGCGCTGCTGCCGCTTGGGACGAGCGCTTGGGAGCGC 1388
|||||
Db 301 TCGCGGCGCTTGGGAGCGCGCGCTGCTGCCGCTTGGGACGAGCGCTTGGGAGCGC 360
QY 1389 TGCACCTTACGCGACGCTGCTGACATGACCGCGCTTACGCTTACGCTTACGCGCATC 1448
|||||
Db 361 TGCACCTTACGCGACGCTGCTGACATGACCGCGCTTACGCTTACGCTTACGCGCATC 420
QY 1449 TGCAGCGCGCTTGGGAGCGCGCGCTGCTGCCGCTTGGGACGAGCGCTTGGGAGCGC 1508
|||||
Db 421 TGCAGCGCGCTTGGGAGCGCGCGCTGCTGCCGCTTGGGACGAGCGCTTGGGAGCGC 480
QY 1509 GTGCTTGGGAGCGCGCTGCTGCTTGGGAGCGCGCGCTTGGGAGCGCGCTTGGGAGC 1568
|||||
Db 481 GTGCTTGGGAGCGCGCTGCTGCTTGGGAGCGCGCGCTTGGGAGCGCGCTTGGGAGC 540
QY 1569 CAGGACCCCGGATCTCGTATGTCGCGGCGCTTGGGAGCGCGCGCTTGGGAGCGCGC 1628
|||||
Db 541 CAGGACCCCGGATCTCGTATGTCGCGGCGCTTGGGAGCGCGCGCTTGGGAGCGCGC 600
QY 1629 CCTCTGCGCTTGGGAGCGCGCTTGGGAGCGCGCGCTTGGGAGCGCGCGCTTGGGAGC 1688
|||||
Db 601 CCTCTGCGCTTGGGAGCGCGCTTGGGAGCGCGCGCTTGGGAGCGCGCGCTTGGGAGC 660
QY 1689 GGGCCCGGAGACCGCGGAGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGCGCGC 1748
|||||
Db 661 GGGCCCGGAGACCGCGGAGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGCGCGC 720
QY 1749 CAGCTGAGCGCGCTGCTGATGCTGAGCGCGCGCTTGGGAGCGCGCGCTTGGGAGCGC 1808
|||||
Db 721 CAGCTGAGCGCGCTGCTGATGCTGAGCGCGCGCTTGGGAGCGCGCGCTTGGGAGCGC 780
QY 1809 CTGTGCTTACGATCTTCTTACGCGGCTCATCGGCGGAGCGCTTGGGAGCGCGCGCGC 1868
|||||
Db 781 CTGTGCTTACGATCTTCTTACGCGGCTCATCGGCGGAGCGCTTGGGAGCGCGCGCGC 840
QY 1869 CTGCGAGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGC 1928
|||||
Db 841 CTGCGAGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGC 900
QY 1929 CGTAATGAGCGCGCGCTTGGGAGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGC 1988
|||||
Db 901 CGTAATGAGCGCGCGCTTGGGAGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGCGC 960
QY 1989 GGGCAAGCGCTGAGTCCCTTCCCGTGGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGC 2048
|||||
Db 961 GGGCAAGCGCTGAGTCCCTTCCCGTGGCGCGCGCGCTTGGGAGCGCGCGCGCTTGGGAGC 1020
QY 2049 --TCTATTTCGATTCGACCTCCACCCGCG 2078

XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
 XX WPI; 2001-355879/37.
 XX P-PSDB; AAB62652.
 XX
 XX Forming reversible peptide receptor complex for purifying cell and
 XX peptides, stimulating signal transduction and modulating hormone
 XX secretion, involves contacting a receptor with zsig33 polypeptide.
 XX
 XX Disclosure; Page 102-104; 111pp; English.
 XX
 XX The invention relates to a method of forming a reversible peptide-
 XX receptor complex that involves providing an immobilized receptor, and
 XX contacting the receptor with a zsig33 peptide (comprising residues 24-37
 XX of AAB62652), where the receptor binds to the zsig33 peptide. The method
 XX is useful for purifying cells, purifying a peptide, stimulating signal
 XX transduction in a cell expressing a receptor. It is also useful for
 XX modulating secretion of hormones, neural development and/or utilization,
 XX gastric contractility, nutrient uptake, secretion of digestive and
 XX pancreatic enzymes and hormones, secretion of insulin-like growth factor
 XX 1, secretion of non-zsig33 proteins. It is useful for modulating growth
 XX hormone secretion in a mammal having a disease associated with abnormal
 XX levels of growth hormone, such as osteoporosis, bone repair, bone
 XX remodeling, low osteoblast levels, cartilage repair and remodeling,
 XX skeletal dysplasia, immune suppression, obesity, growth retardation,
 XX protein catabolic responses after surgery, cachexia, protein loss,
 XX dwarfism, wound healing and ovulation induction, treating a mammal having
 XX a metabolic disorder requiring neurological feedback, such as satiety
 XX regulation, glucose absorption and metabolism and neuropathy-associated
 XX gastrointestinal disorders, and stimulating glucose-induced insulin
 XX release in a mammal. The present sequence represents the DNA encoding the
 XX long form of motilin receptor, GPR-38A (one of the two isoforms of GPR38
 XX which result from alternative splicing). GPR38 has homology to the human
 XX G-protein coupled receptor, GHS-R
 XX
 XX Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;
 XX
 XX Query Match 29.4%; Score 901; DB 4; Length 1239;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-140;
 XX Matches 901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 TCCGCCCCCTCCGCGCCCGCGCTTGGATCAACCCGCGCCGCGTCCGCGCTATCCT 480
 QY 1509 GTGCTCTGGGCGCGTGGCGCTGCTCTGCGCCGCTCTTGTCTCTGCTGGGCTCGAG 1568
 DB 481 GTGCTCTGGGCGCGTGGCGCTGCTCTGCGCCGCTCTTGTCTCTGCTGGGCTCGAG 540
 QY 1569 CAGAACCCCGGCAATCTCCGTATGATCCCGGAGCTCAATGGACCGCGGATCGCTCTCG 1628
 DB 541 CAGAACCCCGGCAATCTCCGTATGATCCCGGAGCTCAATGGACCGCGGATCGCTCTCG 600
 QY 1629 CCTCTCGGCTCGTGGCGCGCTCTGCTCTGCGCGCGCGCAACCGCGCTCCCGCGCTCG 1668
 DB 601 CCTCTCGGCTCGTGGCGCGCTCTGCTCTGCGCGCGCGCAACCGCGCTCCCGCGCTCG 660
 QY 1689 GGGCCCGAGACCGCGGAGCGCGCGCGCTTCAAGCCGGAATCGCGCGCGCGCGCG 1748
 DB 661 GGGCCCGAGACCGCGGAGCGCGCGCGCTTCAAGCCGGAATCGCGCGCGCGCGCG 720
 QY 1749 CAGCTGGGCGCGCTCGCTGATGCTGTGGGTCAACACCGCTTACTTCTCTCTCTT 1808
 DB 721 CAGCTGGGCGCGCTCGCTGATGCTGTGGGTCAACACCGCTTACTTCTCTCTCTT 780
 QY 1809 CTGTGCTCAGACATCTCTCAAGGCTCATCGGCGGAGAGCTGTGAGAGCGCGCGCG 1868
 DB 781 CTGTGCTCAGACATCTCTCAAGGCTCATCGGCGGAGAGCTGTGAGAGCGCGCGCG 840
 QY 1869 CTGCGAGGCGCGCGCGCTCTCGGCGGAGAGAGGCGCAACCGCGAGCTTCGCTCTG 1928
 DB 841 CTGCGAGGCGCGCGCGCTCTCGGCGGAGAGAGGCGCAACCGCGAGCTTCGCTCTG 900
 QY 1929 C 1929
 DB 901 C 901

RESULT 10
 ABR90132
 ID ABR90132 standard; DNA; 1239 BP.
 XX
 XX AC ABR90132;
 XX
 XX 21-OCT-2002 (first entry)
 XX
 XX DNA encoding human G protein-coupled receptor 38 (GPR38).
 XX
 XX Human; G protein-coupled receptor 38; receptor; GPR38; gene; ds;
 XX Alzheimer's disease; Parkinson's disease; ulcerative colitis;
 XX Crohn's disease; Hodgkin's disease; glioblastoma; breast carcinoma;
 XX colon carcinoma; lung small cell carcinoma; lung adenocarcinoma;
 XX pancreatic small cell carcinoma; pancreatic adenocarcinoma.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 1..1239
 XX /*tag= a
 XX /product= "Human G protein-coupled receptor 38 (GPR38)"
 XX
 XX W0200257791-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 29-NOV-2001; 2001WO-US045219.
 XX
 XX 29-NOV-2000; 2000US-0250251P.
 XX
 XX 30-NOV-2000; 2000US-0250452P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 XX Brown JP, Burner GC, Roush CL, Kulanter BG;
 XX WPI; 2002-566812/60.

DR P-PSDB: ABG30936.

XX Assay for detecting Alzheimer's disease, Parkinson's disease, ulcerative
PT colitis, Crohn's disease, Hodgkin's disease, glioblastoma or carcinoma,
XX comprises using a binding partner for G protein coupled receptor 38.

PS Disclosure; Fig 1; 112pp; English.

XX The present invention relates to a new assay method that involves
CC contacting a binding partner specific for G protein coupled receptor
CC (GPR) 38 with specific cells. The method of the invention is useful for
CC the detection of an increased risk of Alzheimer's disease, Parkinson's
CC disease, ulcerative colitis, Crohn's disease, Hodgkin's disease,
CC glioblastoma, or carcinoma. GPR 38 is used to manufacture a medicament
CC for inhibiting, treating or preventing Alzheimer's disease, Parkinson's
CC disease, ulcerative colitis, Crohn's disease, Hodgkin's disease,
CC glioblastoma, breast carcinoma, colon carcinoma, lung small cell
CC carcinoma, lung adenocarcinoma, pancreatic small cell carcinoma, and
CC pancreatic adenocarcinoma. An agonist or antagonist to GPR 38 are used to
CC manufacture a medicament able to reduce the symptoms of these diseases.
CC Nucleic acids encoding GPR 38 can also be used to treat the diseases. The
CC present nucleic acid sequence encodes the human G protein-coupled
CC receptor 38 (GPR38) of the invention

SQ Sequence 1239 BP; 172 A; 431 C; 397 G; 239 T; 0 U; 0 Other;

Query Match 29.4%; Score 901; DB 6; Length 1239;

Best Local Similarity 100.0%; Pred. No. 1,9e-140; Mismatches 0; Gaps 0;

Matches 901; Conservative 0; Indels 0; Gaps 0;

QY 1029 ATGGGACAGCCCTTGGAGACGAGCGAGCGCCCGAGGAGGAGCGCGCGTGGCC 1088
DB 1 ATGGGACAGCCCTTGGAGACGAGCGAGCGCGCCCGAGGAGGAGCGCGCGTGGCC 60
QY 1089 GCGGTGCGCGCTTGGAGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1148
DB 61 GCGGTGCGCGCTTGGAGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 1149 GTGACCGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1208
DB 121 GTGACCGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 1209 ATGCTGATCGGGCGGTATCGGGAGATGCGGACACCACTTGTACTGTGGGAGATG 1268
DB 181 ATGCTGATCGGGCGGTATCGGGAGATGCGGACACCACTTGTACTGTGGGAGATG 240
QY 1269 GCGGTGCGCGCTTGGAGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1328
DB 241 GCGGTGCGCGCTTGGAGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 1329 TCGCGGCGCTTGGAGT 1388
DB 301 TCGCGGCGCTTGGAGT 360
QY 1389 TGCACCTACGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1448
DB 361 TGCACCTACGACGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 1449 TCGCGGCGCTTGGAGT 1508
DB 421 TCGCGGCGCTTGGAGT 480
QY 1509 GTGCTGTGGGCGGT 1568
DB 481 GTGCTGTGGGCGGT 540
QY 1569 CAGGACCCCGGAGATCTCGTAGTCCCGGCGCTCAATGACACCGCGGATCGCTCTCG 1628
DB 541 CAGGACCCCGGAGATCTCGTAGTCCCGGCGCTCAATGACACCGCGGATCGCTCTCG 600
QY 1629 CCTTGTGCTGT 1688
DB 601 CCTTGTGCTGT 660

QY 1689 GGGCCCGAGACCGGAGAGCGCGCGCGCTGTCAAGCCGCAATGCGGCGCGCGCG 1748
DB 661 GGGCCCGAGACCGGAGAGCGCGCGCGCGCTGTCAAGCCGCAATGCGGCGCGCGCG 720
QY 1749 CAGCTGGGCGCGCTGT 1808
DB 721 CAGCTGGGCGCGCTGT 780
QY 1809 CTGTGCTCAGATCTCTTACGAGGCTCATCGGCGGCGGAGCTGTGAGAGCGCGCGCG 1868
DB 781 CTGTGCTCAGATCTCTTACGAGGCTCATCGGCGGCGGAGCTGTGAGAGCGCGCGCG 840
QY 1869 CTGCGAGGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1928
DB 841 CTGCGAGGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 1929 C 1929
DB 901 C 901
RESULT 11
ID AB242842
ID AB242842 standard; DNA; 1239 BP.
XX AB242842;
XX 04-MAR-2003 (first entry)
DE Human motilin receptor GPR38 nucleotide SEQ ID NO:472.
XX
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related disease; cell proliferation-related disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW posttraumatic stress disorder; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
XX Homo sapiens.
OS
XX MO200261087-A2.
XX
XX 08-AUG-2002.
XX
XX 19-DEC-2001; 2001MO-US050107.
XX
XX 19-DEC-2000; 2000US-0257144P.
XX
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
XX Burner GC, Roush CL, Brown JP;
XX
XX WPI; 2003-046718/04.
XX
XX P-PSDB; ABP81993.
XX
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.
XX
XX Disclosure; Fig 1; 523pp; English.
PS
XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or

CC status of many C residues to be determined simultaneously. ABO13410-
 CC ABO14121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 XX

Sequence 1179 BP, 399 A; 443 C; 159 G; 178 T; 0 U; 0 Other;

Query Match 24.8%; Score 761.4; DB 6; Length 1179;
 Best Local Similarity 77.9%; Pred. No. 2.7e-117;
 Matches 918; Conservative 0; Mismatches 261; Indels 0; Gaps 0;

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Qy 588 CAGATCCCTGAGAGTGGCCCGAGTACCAAGTCAAGAAAAGCCCGTCACTGCTCAG 647
Db 1 CAAATCCCTGAGAAAATCCCGAAATACCAAACTAAACAAAAGCCCGTCACTCAG 60
Qy 648 TCCTGTAAACCAAGCTGTAGGTGAGACATGCTCAGCCGAGCCGAGGCTCTGT 707
Db 61 TCCTATAACCAAACTATCTTAATATACAAATGCTCAGCCGAGAAATTAATCTGTA 120
Qy 708 CGCTAAGGCGCCGGTATTCAGTATAGTGAAGAGGAGCGCCCTGGAATGCAATGGC 767
Db 121 CGTAAACCAAGCTGTAGGTGAGACATGCTCAGCCGAGCCGAGGCTCTGT 180
Qy 768 CCGGAGAGCGCCGGAGAGCGAGCATGCGCGGCGCGGCGCGGCGCGGCGGCGG 827
Db 181 CCGAAAAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 828 AGATGCGCGGAGTGTAGTGTGAGAGCGGCTGTGAGAGAGAGAGAGAGAGAGAG 887
Db 241 AAATTAACCGCGAGTGTAGTGTGAGAGCGGCTGTGAGAGAGAGAGAGAGAGAG 300
Qy 888 GCGCGGAGCGAGCGAGCGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 947
Db 301 GCGCGGAGCGAGCGAGCGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 360
Qy 948 GGGAGAGAGCGGCTGTGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1007
Db 361 AAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 1008 CCGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1067
Db 421 CGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 1068 GCGGAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1127
Db 481 AGCGAGAGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 1128 CCGCTGGGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 1187
Db 541 CCGCTAAAAAGCGCTAAATACGATACCGATATACCTATTAATCTATTCGTGAGATA 600
Qy 1188 AGCGGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 1247
Db 601 AAGGAGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 660
Qy 1248 AACTGTGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1307
Db 661 AACTTTATCTAAACAGATACGATACCGATATACCTATTAATCTATTCGTGAGATA 720
Qy 1308 GACTGTGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 1367
Db 721 GACTTTATCTAAACAGATACGATACCGATATACCTATTAATCTATTCGTGAGATA 780
Qy 1368 TCCCTGTAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1427
Db 781 TCCCTGTAGTAAACAGATACGATACCGATATACCTATTAATCTATTCGTGAGATA 840
Qy 1428 GTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1487
Db 841 GTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 1488 GCGGTCGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 1547

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Db 901 CCGGTCGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTGAGAGCGGCTGTG 960
Qy 1548 TGTGTCGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1607
Db 961 TTATTCCTAATAAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1608 ACCGCGGAGATGCTCTCTGCGCTGTGCGCTGTGCGCGGCTGTGCGCTGTGCGG 1667
Db 1021 ACCGCGGAGATGCTCTCTGCGCTGTGCGCTGTGCGCGGCTGTGCGCTGTGCGG 1080
Qy 1668 CCAACCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCGGCTGTG 1727
Db 1081 CCACCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCGGCTGTGCGCGGCTGTG 1140
Qy 1728 GAATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1766
Db 1141 GAATACGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1179

```

RESULT 14
 ABO47149/C
 ID ABO47149 standard; DNA, 1179 BP.
 XX
 AC ABO47149;
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 31740.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 01-SEP-2001; 2001WO-EP010074.
 XX
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PR 05-SEP-2000; 2000DE-0104543.
 XX
 PA (EPIC-) EPICENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K, Guetig D;
 XX
 DR WPI, 2002-371829/40.
 XX
 PT Determining the degree of cytosine methylation in genomic DNA, useful for
 PT diagnosis and prognosis, comprises selective hybridization of amplicons
 PT from chemically treated DNA.
 XX
 PS Claim 12; 56pp + Sequence Listing; 56pp; German.
 XX
 CC This invention describes a novel method for determining the degree of
 CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
 CC genomic sample of DNA. The sample is treated chemically to convert
 CC cytosine (C) but not methylated C, to uracil, then part of the genomic
 CC DNA that contains the target C is amplified to form a labeled amplicon.
 CC The amplicon is hybridised to two classes, each with at least one member,
 CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
 CC degree of hybridisation to both classes is determined from the label on
 CC the amplicon. From the ratio of labels hybridised to the two classes of
 CC oligomers, the degree of methylation is calculated. The method is used:
 CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
 CC and of a wide range of diseases, e.g. cancer, disorders of the central
 CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
 CC particularly by detecting mutations or single nucleotide polymorphisms
 CC (SNP's) and (ii) for differentiation of cell or tissue types and for
 CC investigating cell differentiation. The method allows the methylation

status of many C residues to be determined simultaneously. AB013410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention

Sequence 1179 BP; 462 A; 419 C; 159 G; 139 T; 0 U; 0 other;

Query Match 23.5%; Score 722; DB 6; Length 1179;
Best Local Similarity 75.8%; Pred. No. 9,2e-111;
Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

CC status of many C residues to be determined simultaneously. AB013410-
CC AB054121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
CC
XX
SQ Sequence 1179 BP; 462 A; 419 C; 159 G; 139 T; 0 U; 0 other;
Query Match 23.5%; Score 722; DB 6; Length 1179;
Best Local Similarity 75.8%; Pred. No. 9,2e-111;
Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 589 AGATCCCTTGAAGCTGCTAGGGGTCAGACATGCTACCGGACCGGGGTAGGGCTGTC 648
DB 1178 AGATTTTTCGAAGGTGTCGAGATATTAGATTGATAAAGCGTTCCGTATAGTGTAGT 1119
QY 649 CCTGTACCAAGTGCTAGGGGTCAGACATGCTACCGGACCGGGGTAGGGCTGTC 708
DB 1118 TTTGTAATTAAAGTTGTTAGGGTGAATATATGCTTTATCGATCGGATAGGGTGTGC 1059
QY 709 GCTAAGGCGCCGCGGTATTCAGTTAGTGAAGAGGAGCGCCCTGGAACCTGCATGAGCC 768
DB 1058 GTTAAAGGCGCGCGGTATTTAGTTAGTGAAGAGGAGCGTTTGGATTGTATGGGTT 999
QY 769 CGGAGAGAGGGGCGGAGCGGAGCATGCGCGGCGGGGCGGGCGCGCTTGGCGGA 828
DB 998 CGGAGAGAGGGGCGGAGCGGAGCATGCGCGGCGGGGCGGGCGCGCTTGGCGGA 939
QY 829 GACTGCGGCGAGCTAGCTCGGAGCGGCGCTCGGAGCCACCGCGAGCGGCTTTCGCG 888
DB 938 GATTGCGCGTATGTTAGTTTCGAGACGTTTCGAGTTATTTTCGATAGGATGTTTTCGCG 879
QY 889 CCGCGAGCGGAGCGGAGCGGCTCGCGCTGATCCTCCCGCGCGCGAGCGTGCAGGCTG 948
DB 878 TTTGTAATTAAAGTTGTTAGGGTGAATATATGCTTTATCGATCGGATAGGGTGTGC 819
QY 949 GGAAGAGAGCGGCTCAACGAGAGGAGCAACGCGCGGAGCGCTCCGAGCCCGGAGCGC 1008
DB 818 GGAAGAGAGCGGCTTATCGAGAGGAGATTCACCGTTAGGTTTATGTTTCGATTCGAGAGCG 759
QY 1009 GCGCGCGCGCGGAGCAACCATGAGCCCTCGGAGCGGAGCGGCGCGCGGAGCGG 1068
DB 758 GCGCGTGCAGGAGTATTTAGGAGTATTTTGAAGGAGTATTCGATTCGAGAGCGG 639
QY 1069 CCGCGGAGCGGCGGCGCGCGCGCTCGCGCTGATCCTCCCGCGCGAGCGTGCAGGCTG 1128
DB 698 CCGCGGAGCTGCTGCGGTTGCGGTTGCTTTCGAGAGCGGCTGTTGCTTTT 639
QY 1129 CCTGAGGCGCGCTGCTGCGGTCGACCGCTGTCCTGCTGCTGCTGCTGCGGAGTGA 1188
DB 638 TTTTGGGGGCGTTGGTGTGCTGATCGTATGCTGTTGTTGTTGCTGCTGCGGAGTGA 579
QY 1189 GCGGCAACGTGTGACCTGTATGCTGATCGGGCGCTACCGGAGATGCGGACCAACCA 1248
DB 578 GCGGTAAGTGTGATCGTATGCTGATCGGGCGCTTATCGGAGATGCGGATATTATTTA 519
QY 1249 ACTGTACCTGGGAGCATGAGCCGCTGACCTACTACCTACTGCTGCGGCTGCGCTGCG 1308
DB 518 ATTGTATTTGGGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 459
QY 1309 ACTGTACCGCTTGCAGCTGCGGCGCGCTGCGGCTGCGGCTGCTGCTGCTGCTGCTGCT 1368
DB 458 ATTGTATGCTTTTGGCGCTTGCAGGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399
QY 1369 CCGCTACGTGGGAGGCGGAGCGGAGCTGACGCAACGCTGCTGCAATGACGCGCTGACGC 1428
DB 398 TTTTATGCTGGGAGGAGGCTTGTATTCGTTAGCTTGTATATGATGCGGCTTATGCGC 339
QY 1429 TCGAGCGCTACCTGACCTGCGCGCGCTGCGGCGCGGCTGCTGCTGCTGCTGCTGCTGCT 1488
DB 338 TCGAGCGCTATTTGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
QY 1489 GCGTCCGCGCGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548

DB 278 GCGTTCGCGCGCTTATTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 219
QY 1549 TGTTCCTGTTGGGCGCTGAGAGGAGCCCGGATCTGCTAGTCCCGGCGCTCATATGCA 1608
DB 218 TGTTCCTGTTGGGCGCTGAGAGGAGCCCGGATCTGCTAGTCCCGGCGCTCATATGCA 159
QY 1609 CCGCGGAGTGCCTTCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1668
DB 158 TCGCGCGGATGCTTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCGTTTTCG 99
QY 1669 CACGCGCTGCTGCGGCGGCGGCGGCGGAGACCGCGGAGCGCGGCGCTGCTGAGCGCG 1728
DB 98 TATGCTGCTTTCGTTGCTGCGGCTGCGAGTCCGAGAGTCCGAGGCTGCTGTTTATGCGG 39
QY 1729 AATGCGGCGGAGCGCGCGGAGCTGAGGCGGCTGCTGCT 1766
DB 38 AATGCTGCTGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

RESULT 15
AB047148
ID AB047148 standard; DNA; 1179 BP.
XX
AC AB047148;
XX
DT 12-UTL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 33739.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN MO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001MO-BP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
PA (EPIC-) EPIDENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
XX WPI; 2002-371829/40.
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
XX
PS Claim 12; 56bp + Sequence Listing; 56bp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert in a
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridized to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridization to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridized to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly for detecting mutations or single nucleotide polymorphisms
CC (SNPs); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation

CC Status of many C residues to be determined simultaneously. AB013410-
 CC AB054121 represent genomic DNA sequences used to illustrate the method
 CC for determining the degree of cytosine methylation described in the
 CC disclosure of the invention
 CC
 XX
 SQ Sequence 1179 BP; 139 A; 159 C; 419 G; 462 T; 0 U; 0 Other;

Query March 23.5%; Score 722; DB 6; Length 1179;
 Best Local Similarity 75.8%; Pred. No. 9.2e-111;
 Matches 893; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 589 AGATCCCTTCCGAGGTCGCGGAGTACACAGCTGACCAAAAGCCGCTGACAGTGCAGT 648
 Db 2 AGATTTTTCGAAAGGTGTCGAGTATTAGTATGATTAAGCCGTTCGTATAGTATTAGT 61
 QY 649 CCTGTACCAAGCTGCTAGAGGTGACAGATGCTCAGCCGACCGGGTATGAGCTGTCG 708
 Db 62 TTGTAAATTAAAGTTGTTAGGGGTGATATCGTTATCGATCGGGTATGAGCTGTCG 121
 QY 709 GCTAAGGGGCGCGGGTATTCAGTTAGTGAAGAGGAAAGCCCTGGAACCTGATAGGGGC 768
 Db 122 GTTAAAGGCGTCGCGGTATTTTATGTTAGTGAAGAGGAAAGCTTTTGAATTGTATAGGTT 181
 QY 769 CGGAGAGGGCGCGGAGCGAGAGATGCGGGCCGGGCGGCGCGCGCTGAGCGGA 828
 Db 182 CGGAGAGGGCGCGGAGCGAGAGATGCGGGTCGGGCGGCGCGCTGAGCGGA 241
 QY 829 GACTGCGCGAGCTGCTGAGAGCGCTGAGAGCCGACCCGACAGCGCTTCTGCGG 888
 Db 242 GATTGCGCGTATGTTAGTTCGAGAGCGTTTGGAGATTATTTCTAAGATGCTTTTCGCG 301
 QY 889 CCCCAGCGCAGCGCAGCGCTCCGCGTCTGACTGCGCGCCCGCAGCGTTCGAGGCTG 948
 Db 302 TTTCTAGCGTAGGCTGAGCGCTTTCGTGTTGATTTGTGCGCTTCGAGCGTTCGAGGCTG 361
 QY 949 GGAAGAGAGCGCTCAACGAGAGGACCAAGCGCCGACCGCCGAGCCGCGAGCGC 1008
 Db 362 GGAAGAGAGCGCTTATCGAGAGGATACGCGTATGTTTATGTTATTCGAGCGC 421
 QY 1009 GAGGCGCGCGAGGACCCATGAGGAGCCCTGGAACGAGCGAGCGCCCGCAGAGGAG 1068
 Db 422 GAGGCGCGCGAGGATTTATGAGGATTTTGTGAACGATGAGATCGTTTCGAGGAGG 481
 QY 1069 CGCGGAGCGCGCTGCGCGCTGCGCTGCGCTGCGAGCGAGCGCGCTGCGCTTTC 1128
 Db 482 CGCGGAGCGCTGCTGCTGCGCTGCGCTGCGCTGCGAGCGCGCTGCTGCTTTC 541
 QY 1129 CCGTGGGCGCGCTGCTGCGCGTGAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1188
 Db 542 TTTTGGGCGCGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
 QY 1189 GCGGCAACGTGTGACCGTATGCTATCGGCGCTACCGGACATGCGGACACCA 1248
 Db 602 GCGGTAAAGTGTGATCGTATGCTATCGGCGCTATCGGATATGCGGATTTATTA 661
 QY 1249 ACTTGTACCTGAGGAGAGGCGGTGCGACCTACTCATCTGCTGCGGCTGCGCTGCTG 1308
 Db 662 ATTTGTATTTGAGTATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 721
 QY 1309 ACCGTGACCGCTCTGCGCGTGCAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1368
 Db 722 ATTTGTATGCTTTTGGCGTGCAGGCTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781
 QY 1369 CCTCTACGTGAGGAGGCTGACCTATGCGACAGCTGCTGACATGACCGGCTCAGCG 1428
 Db 782 TTTTTCAGTGGGCGAGGCTGATTTATGATTAAGTTAGTTGATATGATCGCTTATAGCG 841
 QY 1429 TCAGAGCTACCTGAGCATGCGCGCGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 1488
 Db 842 TCAGAGCTATTTGATTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
 QY 1489 GCGTCCGCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1548

Db 902 GCGTCCGCGCTTATCGTGTGTTTGGGTGCGGCGTGTGTTTTCGCTTTCGCTTTCG 961
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 Db 962 TGTTCCTGTGAGGCTCGAGCAGAGATTCGATATTTTCGATATTTTCGAGTTTATAGGA 1021
 QY 1609 CCGCGGATGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTG 1668
 Db 1022 TCGCGGATGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTGCGCTCTG 1081
 QY 1669 CACCGCGTCCCGCGCTGCGGAGCGAGACCGGAGGCGCGCGCTGTTCAAGCGCG 1728
 Db 1082 TATCGTCTTTTCGTCGTCGCGGCTTCAGATCGCGAGGTCGCGCTGTTTATGTCGCG 1141
 QY 1729 AATGCGGCGAGCCCGCGCAGCTGAGCGCGCTGCT 1766
 Db 1142 AATGCGGCGAGTTTCGCTAGTTCGAGGCGCGCTGCT 1179

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OK nucleic - nucleic search, using sw model

Run on: July 17, 2004, 16:52:37 ; Search time 207 Seconds

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	283	9.2	283	3	US-08-993-088A-4 Sequence 4, Appl1
2	283	9.2	283	4	US-08-993-424B-4 Sequence 4, Appl1
3	283	9.2	283	4	US-09-603-680-4 Sequence 4, Appl1
4	248.2	8.1	1050	4	US-09-762-661A-1 Sequence 1, Appl1
5	234.8	7.7	1063	3	US-09-077-675A-1 Sequence 1, Appl1
6	234.8	7.7	1063	4	US-09-077-674-1 Sequence 1, Appl1
7	231.6	7.6	1095	4	US-09-743-475-2 Sequence 2, Appl1
8	231.6	7.6	4009	4	US-09-743-475-1 Sequence 1, Appl1
9	230	7.5	1029	4	US-09-077-675A-4 Sequence 4, Appl1
10	230	7.5	1029	4	US-09-077-674-4 Sequence 4, Appl1
11	229	7.5	250	4	US-09-016-434-359 Sequence 359, App
12	228.8	7.5	1122	3	US-09-077-675A-9 Sequence 9, Appl1
13	228.8	7.5	1122	4	US-09-077-674-9 Sequence 9, Appl1
14	228.4	7.4	1092	4	US-09-077-675A-15 Sequence 15, Appl1
15	228.4	7.4	1092	4	US-09-077-674-15 Sequence 15, Appl1
16	228.4	7.4	3129	4	US-09-077-675A-14 Sequence 14, Appl1
17	228.4	7.4	3129	4	US-09-077-674-14 Sequence 14, Appl1
18	227.8	7.4	1088	3	US-09-077-675A-6 Sequence 6, Appl1
19	227.8	7.4	1088	4	US-09-077-674-6 Sequence 6, Appl1
20	227.8	7.4	1101	4	US-09-016-434-1148 Sequence 1148, Ap
21	227.8	7.4	1101	4	US-09-170-496D-87 Sequence 87, Appl1
22	227.8	7.4	1101	4	US-09-170-496D-209 Sequence 209, Appl
23	227.8	7.4	1101	4	US-09-364-425B-44 Sequence 44, Appl1
24	202.2	6.6	29629	4	US-09-729-995-3 Sequence 3, Appl1
25	202.2	6.6	29629	4	US-10-135-688-3 Sequence 3, Appl1
26	191.8	6.3	111282	4	US-09-758-250-3 Sequence 3, Appl1
27	191	6.2	152331	3	US-09-128-155-16 Sequence 16, Appl1

C 28	189.8	6.2	55298	4	US-09-491-356C-1	Sequence 1, Appl1
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C 31	185.6	6.1	38653	4	US-09-922-445-1	Sequence 1, Appl1
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C 33	185.6	6.1	162450	4	US-09-345-882-1	Sequence 1, Appl1
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C 35	185.4	6.0	7676	2	US-08-451-778A-7	Sequence 7, Appl1
C 36	185.4	6.0	7676	2	US-08-998-208-7	Sequence 7, Appl1
C 37	185.4	6.0	7676	5	PCT-US95-06743-7	Sequence 7, Appl1
C 38	185	6.0	21721	4	US-09-269-938A-41	Sequence 41, Appl1
C 39	185	6.0	22976	4	US-09-269-939A-19	Sequence 19, Appl1
C 40	185	6.0	23187	4	US-09-499-522-1	Sequence 1, Appl1
C 41	185	6.0	128779	4	US-09-497-855A-38	Sequence 38, Appl1
C 42	184.8	6.0	1827	2	US-08-737-371A-3	Sequence 3, Appl1
C 43	184.8	6.0	1827	5	PCT-US95-05853-3	Sequence 3, Appl1
C 44	184.8	6.0	7130	3	US-09-056-105-31	Sequence 31, Appl1
C 45	184.8	6.0	11288	3	US-08-646-301A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-993-088A-4
Sequence 4, Application US/08993088A
Patent No. 6287855
GENERAL INFORMATION:
APPLICANT: Tan, Carina
APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION: GALANIN RECEPTOR GALT2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,088A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/033,851
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 19846
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1958
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
FEATURE:
NAME/KEY: Other
LOCATION: 1...283
OTHER INFORMATION: cDNA probe
US-08-993-088A-4

Query Match 9.2%; Score 283; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1234 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTACTATCTG 1293
DB 1 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTACTATCTG 60
QY 1294 TGGGACCTGCGCTGTGACCTGTACCGCTTGGCGCTGCGGCTTGGGCTTGGGCTG 1353
DB 61 TGGGACCTGCGCTGTGACCTGTACCGCTTGGCGCTGCGGCTTGGGCTTGGGCTG 120
QY 1354 TGTCTGCGGCTGTGCTTCTTACGTCGAGGCTGCACTTACGCGAGCTGCTGACA 1413
DB 121 TGTCTGCGGCTGTGCTTCTTACGTCGAGGCTGCACTTACGCGAGCTGCTGACA 180
QY 1414 TGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1473
DB 181 TGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 240
QY 1474 TGTGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1516
DB 241 TGTGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 283

RESULT 2
US-08-993-424B-4
; Sequence 4, Application US/08993424B
; Patent No. 6337206
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Kolakowski, Lee F., Jr.
; TITLE OF INVENTION: MOUSE GALANTIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,424B
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846NP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...283
; OTHER INFORMATION: cDNA probe

US-08-993-424B-4
Query Match 9.2%; Score 283; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1234 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTACTATCTG 1293
DB 1 TGGGACACACCACTTGTACCTGGGACAGATGCGGCTGCACTTACTATCTG 60
QY 1294 TGGGACCTGCGCTGTGACCTGTACCGCTTGGCGCTGCGGCTTGGGCTTGGGCTG 1353
DB 61 TGGGACCTGCGCTGTGACCTGTACCGCTTGGCGCTGCGGCTTGGGCTTGGGCTG 120
QY 1354 TGTCTGCGGCTGTGCTTCTTACGTCGAGGCTGCACTTACGCGAGCTGCTGACA 1413
DB 121 TGTCTGCGGCTGTGCTTCTTACGTCGAGGCTGCACTTACGCGAGCTGCTGACA 180
QY 1414 TGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1473
DB 181 TGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 240
QY 1474 TGTGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1516
DB 241 TGTGACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 283

RESULT 3
US-09-603-680-4
; Sequence 4, Application US/09603680
; Patent No. 6544753
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANTIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/603,680
; FILING DATE: 26-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846 CA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other

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FEATURE:
NAME/KEY: Other
LOCATION: 1...283
OTHER INFORMATION: cdna probe
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-603-680-4

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Query Match          9.2%; Score 283; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.5e-47;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1234 TGGCGACCACTTGTGACCTGAGCGAGAGCGGCGGCTGCGACCTGACCTGCTGCG 1293
DB 1 TGGCGACCACTTGTGACCTGAGCGAGAGCGGCGGCTGCGACCTGACCTGCTGCG 60
QY 1294 TGGCGCTGCGCTGAGCGGCTGAGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG 1353
DB 61 TGGCGCTGCGGCTTGAAGCTGAGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGG 120
QY 1354 TGGCTGCGGCGGCTTGGCTTCTGAGTGAGCGAGCGGCTGAGCGGCTGAGCGG 1413
DB 121 TGGCTGCGGCGGCTTGGCTTCTGAGTGAGCGAGCGGCTGAGCGGCTGAGCGG 180
QY 1414 TGAACCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 1473
DB 181 TGAACCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 240
QY 1474 TGGTACCGCGGCGGCGGCTGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1516
DB 241 TGGTACCGCGGCGGCGGCTGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGG 283

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RESULT 4
US-09-762-661A-1
; Sequence 1, Application US/09762661A
; Patent No. 6645726
; GENERAL INFORMATION:
; APPLICANT: Howard, Andrew D.
; APPLICANT: Palyha, Oksana C.
; APPLICANT: Smith, Roy G.
; APPLICANT: Tan, Carina P.
; TITLE OF INVENTION: CANINE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20207P
; CURRENT APPLICATION NUMBER: US/09/762,661A
; CURRENT FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/17915
; PRIOR FILING DATE: 1999-08-06
; PRIOR APPLICATION NUMBER: 60/095,960
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1050)
; OTHER INFORMATION: n = A,T,C or G
US-09-762-661A-1

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Query Match          8.1%; Score 248.2; DB 4; Length 1050;
Best Local Similarity 65.9%; Pred. No. 1.9e-40;
Matches 375; Conservative 0; Mismatches 193; Indels 1; Gaps 1;

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QY 1120 CGCCCTTCCCTGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1119
DB 56 CGCTGTTCCTCCCGCGCGCTGCTGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGG 115
QY 1180 TCGGGGTGAGCGGCAAGTGTGACCGGCTGATGCTGAGCGGCGCTACCGGGA 1239
DB 116 TGGGCGTCCGCGGCAAGTGTGACCGGCTGATGCTGAGCGGCGCTACCGGGA 175

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QY 1240 CCACCAACAACTTGTGACCTGAGCGAGAGCGGCTGCGACCTGACCTGCTGCG 1299
DB 176 CCACCAACAACTTGTGACCTGAGCGAGAGCGGCTGCGACCTGACCTGCTGCTGCA 235
QY 1300 TGGCGTGAAGCTGAGCGGCTTGGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1359
DB 236 TGGCGTGAAGCTGAGCGGCTTGGCGGCTGAGCGGCTGAGCGGCTGAGCGG 295
QY 1360 GCGCGCTGCTTCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1419
DB 296 GCGCGCTGCTTCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 355
QY 1420 CGCTAGCGCTGAGCGGCTTACCTGAGCGGCTTACCTGAGCGGCTTACCTGAG 1479
DB 356 CGCTAGCGCTGAGCGGCTTACCTGAGCGGCTTACCTGAGCGGCTTACCTGAG 415
QY 1480 CCGGCGCGGCTGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1539
DB 416 CCGGCGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 475
QY 1540 GTCCCTTCTTGTCTGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 1598
DB 476 GTCCCTTCTTGTCTGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 535
QY 1599 CTCAATGAGCAAGCGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1658
DB 536 GCGAGTCCGCGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 595
QY 1659 TCGCGGCGGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 1687
DB 596 TCGCGGCGGCGGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGG 624

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```

RESULT 5
US-09-077-675A-1
; Sequence 1, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Reighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:

```

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1063 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-675A-1

Query Match 7.7%; Score 234.8; DB 3; Length 1063;
Best Local Similarity 69.3%; Pred. No. 8.6e-38;
Matches 320; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

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QY 1120 GCGCTTTCCCTGAGGCGCGTGTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 1179
DB 69 GCGCTTTCCCTGAGGCGCGTGTGCGCGGTGACCGCGCTGTGTGCTGTGCTGTGCTG 128
QY 1180 TCGGGGTGAGGCGGACAGTGTGTGACCGGATGCTGATCGGCGCTACCGGGAGATGGCA 1239
DB 129 TGGGATGCGGGGCACTGTCTACGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 188
QY 1240 CCACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1299
DB 189 CCACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 248
QY 1300 TGGCGTTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1359
DB 249 TGGCGTTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 308
QY 1360 GCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1419
DB 309 GCAAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 368
QY 1420 CGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1479
DB 369 CGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 428
QY 1480 CCGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1539
DB 429 CCGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 488
QY 1540 GTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1581
DB 489 GCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 530
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RESULT 6

US-09-077-674-1
Sequence 1, Application US/09077674
Patent No. 6531314

GENERAL INFORMATION:

APPLICANT: Arena, Joseph P.
APPLICANT: Cully, Doris F.
APPLICANT: Feighner, Scott D.
APPLICANT: Howard, Andrew D.
APPLICANT: Liberator, Paul A.
APPLICANT: Schaeffer, James M.
APPLICANT: Van der Ploeg, Leonardus
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/077.674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19589P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1063 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-674-1

Query Match 7.7%; Score 234.8; DB 4; Length 1063;
Best Local Similarity 69.3%; Pred. No. 8.6e-38;
Matches 320; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

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QY 1120 GCGCTTTCCCTGAGGCGCGTGTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 1179
DB 69 GCGCTTTCCCTGAGGCGCGTGTGCGCGGTGACCGCGCTGTGTGCTGTGCTGTGCTG 128
QY 1180 TCGGGGTGAGGCGGACAGTGTGTGACCGGATGCTGATCGGCGCTACCGGGAGATGGCA 1239
DB 129 TGGGATGCGGGGCACTGTCTACGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 188
QY 1240 CCACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1299
DB 189 CCACCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 248
QY 1300 TGGCGTTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1359
DB 249 TGGCGTTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 308
QY 1360 GCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1419
DB 309 GCAAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 368
QY 1420 CGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1479
DB 369 CGCTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 428
QY 1480 CCGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1539
DB 429 CCGCGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 488
QY 1540 GTCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1581
DB 489 GCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 530
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RESULT 7

US-09-743-475-2
Sequence 2, Application US/09743475
Patent No. 6682908

GENERAL INFORMATION:

APPLICANT: Smith, Roy G.
APPLICANT: Van der Ploeg, Leonardus H. T.
APPLICANT: Howard, Andrew D.
APPLICANT: Zheng, Hui
APPLICANT: McKee, Karen Kulju
APPLICANT: Jiang, Michael M.
TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
RECEPTOR

```

; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-2

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Query Match      7.6%; Score 231.6; DB 4; Length 1095;
Best Local Similarity 68.8%; Pred. No. 3.8e-37;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 1120 CGCCCTTCCCTGGGGGCGCTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 1179
DB 104 CACTGTTCCTCCGCGCGCGCTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 163
QY 1180 TCGGGGTGAGCGGCAAGTGTGACCGTGAATGCTGATCGGGCGCTACCGGACATGCGGA 1239
DB 164 TGGGCATCTCGGGCAACTGTCTACACATGCTGTGTGTGCTGCTGCTGCGGAGCTGCGCA 223
QY 1240 CCACCACTTCTTACTTCTGAGGAGCAATGAGCGCTGTGCTGCTGCTGCTGCTGCTG 1299
DB 224 CCACCACTTCTTACTTCTGAGGAGCAATGAGCGCTGTGCTGCTGCTGCTGCTGCTG 283
QY 1300 TGGCGTTCGACCTTACCGCGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 1359
DB 284 TGGCGTTCGACCTTACCGCGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 343
QY 1360 GCGCGCTTCCTTCTTACGTTGAGGAGCGCTGCACTGACGCGCTGCTGCTGCTGCTG 1419
DB 344 GCAAACTTCTTCAATTGTCAGAGAGAGCTGCACTGACGCGCTGCTGCTGCTGCTG 403
QY 1420 CGCTCAGGTCGAGCGCTTACTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 1479
DB 404 CGCTCAGGTCGAGCGCTTACTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 463
QY 1480 CCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 1539
DB 464 CCAAGGCGCGCTGAGAGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
QY 1540 GTCCCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1581
DB 524 GCGCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 565

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RESULT 8
US-09-743-475-1
; Sequence 1, Application US/09743475
; Patent No. 6682908
; GENERAL INFORMATION:
; APPLICANT: Smith, Roy G.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Zheng, Hui
; APPLICANT: McKee, Karen Kulju
; APPLICANT: Jiang, Michael M.
; TITLE OF INVENTION: MOUSE GROWTH HORMONE SECRETAGOGUE
; FILE REFERENCE: 20218P
; CURRENT APPLICATION NUMBER: US/09/743,475
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US99/15375
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/092,361
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4009
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-743-475-1

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Query Match      7.6%; Score 231.6; DB 4; Length 4009;
Best Local Similarity 68.8%; Pred. No. 5.7e-37;
Matches 318; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

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QY 1120 CGCCCTTCCCTGGGGGCGCTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 1179
DB 605 CACTGTTCCTCCGCGCGCGCTGCTGCGCGGTGACCGCTGTGTGCTGTGCTGTGCTG 664
QY 1180 TCGGGGTGAGCGGCAAGTGTGACCGTGAATGCTGATCGGGCGCTACCGGACATGCGGA 1239
DB 665 TGGGCATCTCGGGCAACTGTCTACACATGCTGTGTGTGCTGCTGCTGCGGAGCTGCGCA 724
QY 1240 CCACCACTTCTTACTTCTGAGGAGCAATGAGCGCTGTGCTGCTGCTGCTGCTGCTG 1299
DB 725 CCACCACTTCTTACTTCTGAGGAGCAATGAGCGCTGTGCTGCTGCTGCTGCTGCTG 784
QY 1300 TGGCGTTCGACCTTACCGCGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 1359
DB 785 TGGCGTTCGACCTTACCGCGCTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 844
QY 1360 GCGCGCTTCCTTCTTACGTTGAGGAGCGCTGCACTGACGCGCTGCTGCTGCTGCTG 1419
DB 845 GCAAACTTCTTCAATTGTCAGAGAGAGCTGCACTGACGCGCTGCTGCTGCTGCTG 904
QY 1420 CGCTCAGGTCGAGCGCTTACTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 1479
DB 905 CGCTCAGGTCGAGCGCTTACTGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTG 964
QY 1480 CCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCG 1539
DB 965 CCAAGGCGCGCTGAGAGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024
QY 1540 GTCCCTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1581
DB 1025 GCGCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1066

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RESULT 9
US-09-077-675A-4
; Sequence 4, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pal, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-077-675A-4

Query Match 7.5%; Score 230; DB 3; Length 1029;
Best Local Similarity 68.6%; Pred. No. 7.7e-37;
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 1120 CGCCCTTCCCTGGGGGCGCTGGTGGCGGTGACCGCGTGTGCTGTGCTGTGCTG 1179
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QY 1180 TCGGGGTGAGCGGCAAGTGTGACCTGTATCTGATCGGGCGCTTACCGGACATGCGA 1239
DB 326 TGGGTATCGCGGGCAACTGTCTCAAGATGTGTAGTGTACCGCTTCCGAGATGCGCA 385
QY 1240 CCACCAACAATTGTACTGGGAGCATGAGCGGTGTCCGACTACTCATCTGCTGCGGC 1299
DB 386 CCACCAACAACCTTACTCTTCAAGATGTGTAGTGTGTCTTCCGAACTACTTCTTGTGA 445
QY 1300 TGGCGTGTGACCTGTACCGCTTCTGGCGCTGCGCGCTTGGGTGTTCGGGCGCTGTCT 1359
DB 446 TGGCGTGTGACCTTCTTCCGCTTGGGAGTACCGGCTTGGAACTTGGCAACTGTCT 505
QY 1360 GCGCGCTGTCCCTCTACGTGGGGGAGGGGTGACCTTACGCAAGCGTGCATATACCG 1419
DB 506 GCAAACTCTTCCAGTTGTGAGGAGTGTGACCTTACGCAAGCGTGCATATATACCG 565
QY 1420 CGCTCAGCGTGAAGCGCTTACCTGCGCATTCGCGCGCTGCGCGCTGCTTGTGCA 1479
DB 566 CGCTGACGTGTGAGCGCTTCTTCCGCTTGGGAGTGTGAGTGTGCA 625
QY 1480 CCGCGCGCGCGCTGCGCGCTGCTGCTGTGCTGTGCGCGCTGCTGTGCGG 1539
DB 626 CCAAGGCGCGGTAAGCTGTGTCTGTGCTGTGCGCGCTTGTGAGGCGG 685
QY 1540 GTCCCTTCTTGTCTGCTGTGAGCGTGCAGAGGACCGCGCA 1581
DB 686 GGCCCATCTTGT 727

RESULT 10
US-09-077-674-4
Sequence 4, Application us/09077674
Patent No. 653134

GENERAL INFORMATION:

APPLICANT: Arena, Joseph P.
APPLICANT: Cully, Doris F.
APPLICANT: Feigheimer, Scott D.
APPLICANT: Howard, Andrew D.
APPLICANT: Liberator, Paul A.
APPLICANT: Schaeffer, James M.
APPLICANT: Van Der Ploeg, Leonardus
TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.

CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/09/077,674
FILING DATE: 3-JUN-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-077-674-4

Query Match 7.5%; Score 230; DB 4; Length 1029;
Best Local Similarity 68.6%; Pred. No. 7.7e-37;
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

QY 1120 CGCCCTTCCCTGGGGGCGCTGGTGGCGGTGACCGCGTGTGCTGTGCTGTGCTG 1179
DB 266 CGCTCTTCCCGACGCGCTGTGGCGGGCGTCAACCGCACTGCGTGGCGCTTCTGTG 325
QY 1180 TCGGGGTGAGCGGCAAGTGTGACCTGTATCTGATCGGGCGCTTACCGGACATGCGA 1239
DB 326 TGGGTATCGCGGGCAACTGTCTCAAGATGTGTAGTGTGTCTTCCGAGATGCGCA 385
QY 1240 CCACCAACAATTGTACTGGGAGCATGAGCGGTGTCCGACTACTCATCTGCTGCGGC 1299
DB 386 CCACCAACAACCTTACTCTTCAAGATGTGTAGTGTGTCTTCCGAACTACTTCTTGTGA 445
QY 1300 TGGCGTGTGACCTGTACCGCTTCTGGCGCTGCGCGCTTGGGTGTTCGGGCGCTGTCT 1359
DB 446 TGGCGTGTGACCTTCTTCCGCTTGGGAGTACCGGCTTGGAACTTGGCAACTGTCT 505
QY 1360 GCGCGCTGTCCCTCTACGTGGGGGAGGGGTGACCTTACGCAAGCGTGCATATACCG 1419
DB 506 GCAAACTCTTCCAGTTGTGAGGAGTGTGACCTTACGCAAGCGTGCATATATACCG 565
QY 1420 CGCTCAGCGTGAAGCGCTTACCTGCGCATTCGCGCGCTGCGCGCTGCTTGTGCA 1479
DB 566 CGCTGACGTGTGAGCGCTTCTTCCGCTTGGGAGTGTGAGTGTGCA 625
QY 1480 CCGCGCGCGCGCTGCGCGCTGCTGCTGTGCTGTGCGCGCTGCTGTGCGG 1539
DB 626 CCAAGGCGCGGTAAGCTGTGTCTGTGCTGTGCGCGCTTGTGAGGCGG 685
QY 1540 GTCCCTTCTTGTCTGCTGTGAGCGTGCAGAGGACCGCGCA 1581
DB 686 GGCCCATCTTGT 727

RESULT 11
US-09-016-434-359
Sequence 359, Application us/09016434

Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 359:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THPINOT01
CLONE: 2018536
US-09-016-434-359

Query Match 7.5%; Score 229; DB 4; Length 250;

Best Local Similarity 98.8%; Pred. No. 7.7e-37; Mismatches 2; Indels 1; Gaps 1;

Matches 240; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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1 TCTCAGTACTTAACATGCTGCTGCACTTTCTATCTGAGCGCATCAACCA 60
2884 ATCTCTAACACCTCAATTTCAAAGAGTACAGAGCGCGGCTTTAACTGCTGCA 2943
61 ATCTCTAACACCTCAATTTCAAAGAGTACAGAGCGCGGCTTTAACTGCTGCA 120
2944 AGAAGTCCAGGCGAGGAGGCTTCCACAGAGGAGGACACTGCGGGGGAAGTTGACGG 3003
121 AGAAGTCCAGGCGAGGAGG- TTCCACAGAGGAGGAGGACTGCGGGGGAAGTTGACGG 179
3004 GACACTGAGAGAGACCGGTGGGTACACCGAGCAACCGGCTAACTGTAAGCAGTGGGA 3063
180 GACACTGAGAGAGACCGGTGGGTACACCGAGCAACCGGCTAACTGTAAGCAGTGGGA 239
3064 TAA 3066
240 TAA 242

RESULT 12
US-09-077-675A-9
Sequence 9, Application US/09077675A

Patent No. 6242199
GENERAL INFORMATION:
APPLICANT: Pai, Lee-Yuh
APPLICANT: Feilchner, Scott C.
APPLICANT: Howard, Andrew D.
APPLICANT: Pong, Sheng-Shung
APPLICANT: Van Der Ploeg, Leonardus H.T.
TITLE OF INVENTION: RECEPTOR ASSAY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/077,675A
FILING DATE: 3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-675A-9

Query Match 7.5%; Score 228.8; DB 3; Length 1122;

Best Local Similarity 57.9%; Pred. No. 1.4e-36; Mismatches 307; Indels 1; Gaps 1;

Matches 424; Conservative 0; Mismatches 307; Indels 1; Gaps 1;

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360 GCGCTTCCCTGCGGGGCGCTGCGCGGTGACCGCTGTGCTGTGCTGTGCTGT 419
1181 CGGGTGAAGCGGCAAGTGTATCGTATCGGCGGCTTACCGGGAATGCGGAC 1240
420 GGGTATCGGTGCAACCTGCTCAACATGCTGTGTGCTGCGCTTCCGGAAGTGCAC 479
1241 CACCAACAATTGTACTGGGAGAGTGGCGGCTGTCCGACTACTACTACTCTGCGGCT 1300
480 CACCAACAATTGTACTGGGAGAGTGGCGGCTGTCCGACTACTACTACTCTGCGGCT 539
1301 GCGGTGCACTGTATACCGCTCTGCGGCTGCGGCGGCTGTGCTGTGCTGTG 1360
540 GCGGTGCACTGTATACCGCTCTGCGGCTGCGGCGGCTGTGCTGTGCTGTG 599
1361 CGGCTGTGCTGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1420
600 CAACTCTTCCAACTGTGAGTGAAGCTGCACTGAGGAGGAGGAGGAGGAGGAGG 659
1421 GCTCAGCGTGAAGCGGTACTGCGCATCTGCGGCGGCTGCGGCGGCGGCTGTGCT 1480
660 GCTCAGCGTGAAGCGGTACTGCGCATCTGCGGCGGCTGCGGCGGCGGCGGCTGT 719

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Db 720 CAGGGGGCGGGTGAAGAGCTGTGATCTTGTCTATCTTGGGCGGTGGCTTCTGAGCGCCGG 779
OY 1541 TCCCTTCTGTTTCTCTGTGTGGCGGTGAGCAGAGACCCCGCATCT-CCGTAGTCCCGGGCC 1539
Db 780 GCGCCATCTTCGCTAGTGTGGGGTGGAGCAAGAGACGGCACCCGACCTTGGGACACCA 839
OY 1600 TCAATGGGACCGCGGGGANTGCGCTCTGCGCTCTGCGCTGCTGCGCGCTCTGCGCTCT 1639
Db 840 CGAGTGCGCGCCCGACCGAGTTGGGGTGGAGTGTGCTGAGTGTCTCAAGTGTATGTGTGGT 899
OY 1660 CGCGGCGCGCACCGCGCGTCCCGCGCGGTGGGGCCGAGACCGCGAGGCGCGCGCTGT 1719
Db 900 GTCCAGCATCTTCTTCTTCTTCTCTGCTCTGCTGTCTAGCGGTCCTAGCATCTCATGCG 959
OY 1720 TCAGCGCGGAATCGCGCGCCGAGCCCGCGCAGCTGGCGCGCTGCGTGTCA TGTGTGGG 1779
Db 960 CAGGAAGGTGTGGCGGAGAGAGCGGGGAGATGTCTGTGTGGTGTCTGTCTGCTCAGGGACA 1019
OY 1780 TCACCACGCGCTTACTTCTCTGCGCTTCTGTGTGCTCAGGATCCTTACGGGCTCATG 1839
Db 1020 GACCCACAGCAACCGGTGAATAATGCTGTGGTGTCTGAGCGCGCGCTCAGGCTTCTCT 1079
OY 1840 GCGCGGAGCTGT 1851
Db 1080 CGCGGCTCTAT 1091

RESULT 13
US-09-077-674-9
/ Sequence 9, Application US/09077674
/ Patent No. 6531314
/ GENERAL INFORMATION:
/ APPLICANT: Arena, Joseph P.
/ APPLICANT: Gully, Doris P.
/ APPLICANT: Reighner, Scott D.
/ APPLICANT: Howard, Andrew D.
/ APPLICANT: Liberator, Paul A.
/ APPLICANT: Schaeffer, James M.
/ APPLICANT: Van Der Ploeg, Leonardus
/ TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR FAMILY
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Merck & Co., Inc.
/ STREET: P.O. Box 2000, 126 E. Lincoln Ave.
/ CITY: Rahway
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07065-0900
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: Fastseq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/077,674
/ FILING DATE: 3-JUN-1998
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cocuzzo, Anna L.
/ REGISTRATION NUMBER: 42,452
/ REFERENCE/DOCKET NUMBER: 19589P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 732-594-1273
/ TELEFAX: 732-594-4720
/ TELEX:
/ INFORMATION FOR SEQ. ID NO.: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1122 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-077-674-9

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Query Match	7.5%	Score 228.8;	DB 4;	Length 1122;
Best Local Similarity	57.9%	Pred. No. 1.4e-36;		
Matches 424;	Conservative 0;	Mismatches 307;	Indels 1;	Gaps 1;

QY	1122	GGCCCTTCCCTCCG6666GGCTGGAGCCGGAGTGAACCGCGTGGTGGCTGGCTGGCTGGTGGT	1180
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QY	1301	GGCGTTGACCTGTAACCGGCTCTGG6GCTTGCG6GCTTGCG6GCTTG66GCTGGCTCTG	1360
Db	540	GGCCCTGAGACTCGGCTGGCGCTTGG6AGTACCG6GCTTGAACTTGG6GACCTCTCTG	599
QY	1361	CGCGCTGGCCGCTACGAGG6666GAGG66GTCGACATAGCGCAGGCTGGTGGACATAGACCGC	1420
Db	600	CAATCTTTCGAATTCGTGATGAGTGAAGTGAACCTTACGACAGG6TGTACATCATACAGC	659
QY	1421	GCTGACGCTGAGAGGCTACCTGGCACTGTGCGCGCTCGCGGCTCGG6GCGCGGCTTGGTCA	1480
Db	660	GCTGAGCGTCAAGGAGCTACTTGGCACTGTCTTCCACTCGG6GCAAGTGGTGGTCA	719
QY	1481	CGG6GCGCGGCTCCGCGCGCTCATCGCTGGTGGTGGGCGG6GCGTGGCTCTGCGCGG	1540
Db	720	CAG666GCGG6TGAAGCTGGTCACTTTCGTGATCTGG6GCGG6GCTTGTGAGGCGCGG	779
QY	1541	TCCCTTCTTGTCTGTGGTGG6GCTGAGACAGAACCCCGGCACTCTCGTACGCCG6GC	1599
Db	780	GCCCATCTTGTGCTAGTCG666TGGAGNAGCAAGAAAGGCAACGACCTTGG6ACACCA	839
QY	1600	TCAATG6GACG6GCGGAGATGCGCTCTCGGCTCTGCGCTCTGGTGGCGGCTCTGGCTCT	1659
Db	840	CGAGTGGCGGCCCCACGAGTTTGGGTCGCTTGGACTGTCAAGGTATAGTGGTGGT	899
QY	1660	CGCGG6GCGCAACGACGCTGCCGCGCGCTGG66GCGGAGCCGAGACCGCGAGG6CGCGGCGCTGT	1719
Db	900	GTCAGCATCTTCTTCTTCTCTGTCTGTCTGTCTGTCTGTCAAGTCCCTGACAGTCCATGCG	959
QY	1720	TCAAGCCGGAATGCGGCGGACGCCCCGCGGAGTGGGCGGCTGGGTGTCACTGTGGG	1779
Db	960	CAGGAAGTGTGGGAGGAGGCGGAGCATGTGTGTGTGGTGGTCTGTGCTAGAGGACA	1019
QY	1780	TCACCAACGAGCTACTTCTTCTGCTCCCTTCTGTGACTCAGCATTCCTTACG6GCTCATCG	1839
Db	1020	GAAACCAAGCAAACTGTAAATGTGGTGGTGTCTGACGCGGCTCAG6CTTTCCT	1079
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US-09-077-675A-15
; Sequence 15, Application US/09077675A
; Patent No. 6242199
;
; GENERAL INFORMATION:
;
; APPLICANT:  Pai, Lee-Yuh
; APPLICANT:  Feilshner, Scott C.
; APPLICANT:  Howard, Andrew D.
; APPLICANT:  Pong, Sheng-Shung
; APPLICANT:  Van Der Ploeg, Leonardus H.T

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Db 344 GCAAACTCTTCCAGTTGTGACGAGAGCTGACCTAGCCACGGTCTCACCATCAACCG 403
QY 1420 CGCTCAGCGTCGAGCGCTACCTGSCCATCTGCCCCCGCTCCGGCCCCGCGCTTGGTCA 1479
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QY 1480 CCGGGCGCGCGCTCCGGCGCTCATCGCTGTGCTGTGGGCCGTGGCGCTGTCTCTGCGG 1539
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Maximum Match 100%

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SUMMARIES

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3	2021.2	65.9	2040	17	US-10-723-955-129 Sequence 129, App
4	2013.2	65.7	2040	16	US-10-417-820A-151 Sequence 151, App
5	2013.2	29.4	1239	15	US-10-235-567A-472 Sequence 472, App
6	2013.2	29.4	1239	15	US-10-280-078-13 Sequence 13, App
7	2013.2	29.4	1239	15	US-10-280-078-14 Sequence 14, App
8	2013.2	29.4	1239	15	US-10-206-677-1 Sequence 1, App
9	2013.2	29.4	1239	15	US-10-303-204A-1 Sequence 1, App
10	2013.2	29.4	1239	15	US-10-303-204A-4 Sequence 4, App
11	2013.2	29.4	1239	15	US-10-305-720-359 Sequence 359, App
12	2013.2	29.4	1239	15	US-10-225-567A-139 Sequence 139, App
13	2013.2	29.4	1239	15	US-10-303-204A-9 Sequence 9, App
14	2013.2	29.4	1239	15	US-10-303-204A-15 Sequence 15, App

15	228.4	7.4	3129	15	US-10-303-204A-14	Sequence 14, App
16	227.8	7.4	1088	15	US-10-303-204A-6	Sequence 6, App
17	227.8	7.4	1101	15	US-10-251-385-87	Sequence 87, App
18	227.8	7.4	1101	15	US-10-251-385-209	Sequence 209, App
19	227.8	7.4	1101	15	US-10-276-392-22	Sequence 22, App
20	227.8	7.4	1101	16	US-10-305-720-1148	Sequence 1148, App
21	205.2	6.7	5157	9	US-09-764-877-2605	Sequence 2605, App
22	205.2	6.7	5157	16	US-10-242-515-2605	Sequence 2605, App
23	205.2	6.7	5199	9	US-09-764-877-2607	Sequence 2607, App
24	205.2	6.7	5199	16	US-10-242-515-2607	Sequence 2607, App
25	202.2	6.6	29629	14	US-10-135-689-3	Sequence 3, App
26	202.2	6.6	29629	17	US-10-690-617-3	Sequence 3, App
27	201.8	6.6	12822	9	US-09-764-847-1579	Sequence 1579, App
28	201.8	6.6	12822	15	US-10-032-154-1579	Sequence 1579, App
29	201.2	6.6	953	13	US-10-027-632-248867	Sequence 248867, App
30	201.2	6.6	953	16	US-10-027-632-248867	Sequence 248867, App
31	200.8	6.5	704	13	US-10-027-632-125989	Sequence 125989, App
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33	200.4	6.5	39768	13	US-10-087-192-1030	Sequence 1030, App
34	200	6.5	953	13	US-10-027-632-248866	Sequence 248866, App
35	200	6.5	953	13	US-10-027-632-248870	Sequence 248870, App
36	200	6.5	953	16	US-10-027-632-248866	Sequence 248866, App
37	200	6.5	953	16	US-10-027-632-248870	Sequence 248870, App
38	200	6.5	39148	13	US-10-087-192-46	Sequence 46, App
39	199.8	6.5	1920	16	US-10-094-749-198	Sequence 198, App
40	199.6	6.5	704	13	US-10-027-632-125990	Sequence 125990, App
41	199.6	6.5	704	13	US-10-027-632-125991	Sequence 125991, App
42	199.6	6.5	704	13	US-10-027-632-125992	Sequence 125992, App
43	199.6	6.5	704	16	US-10-027-632-125990	Sequence 125990, App
44	199.6	6.5	704	16	US-10-027-632-125991	Sequence 125991, App
45	199.6	6.5	704	16	US-10-027-632-125992	Sequence 125992, App

ALIGNMENTS

RESULT 1

US-09-876-252-129

Sequence 129, Application US/09876252

PUBLICATION NO. US20030018182A1

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.

APPLICANT: Lehmann-Bruinsma, Karin

APPLICANT: Chalmers, Derek T.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Lin, I-Lin

APPLICANT: Dang, Huong T.

APPLICANT: Chen, Ruoping

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re

FILE REFERENCE: AREN-0054

CURRENT APPLICATION NUMBER: US/09/876,252

CURRENT FILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: 09/416,760

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 09/170,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 60/110,060

PRIOR FILING DATE: 1998-11-27

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,852

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/109,213

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/123,944

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,945

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,948

PRIOR FILING DATE: 1999-03-12

PRIOR APPLICATION NUMBER: 60/123,951

PRIOR FILING DATE: 1999-03-12

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1      / PRIOR APPLICATION NUMBER: 60/123,946
2      / PRIOR FILING DATE: 1999-03-12
3      / PRIOR APPLICATION NUMBER: 60/123,949
4      / PRIOR FILING DATE: 1999-03-12
5      / PRIOR APPLICATION NUMBER: 60/152,524
6      / PRIOR FILING DATE: 1999-09-03
7      / PRIOR APPLICATION NUMBER: 60/151,114
8      / PRIOR FILING DATE: 1999-08-27
9      / PRIOR APPLICATION NUMBER: 60/108,029
10     / PRIOR FILING DATE: 1998-11-12
11     / PRIOR APPLICATION NUMBER: 60/136,436
12     / PRIOR FILING DATE: 1999-05-28
13     / PRIOR APPLICATION NUMBER: 60/136,439
14     / PRIOR FILING DATE: 1999-05-28
15     / PRIOR APPLICATION NUMBER: 60/136,567
16     / PRIOR FILING DATE: 1999-05-28
17     / PRIOR APPLICATION NUMBER: 60/137,127
18     / PRIOR FILING DATE: 1999-05-28
19     / PRIOR APPLICATION NUMBER: 60/137,131
20     / PRIOR FILING DATE: 1999-05-28
21     / PRIOR APPLICATION NUMBER: 60/141,448
22     / PRIOR FILING DATE: 1999-06-29
23     / PRIOR APPLICATION NUMBER: 60/136,437
24     / PRIOR FILING DATE: 1999-05-28
25     / PRIOR APPLICATION NUMBER: 60/156,555
26     / PRIOR FILING DATE: 1999-09-29
27     / PRIOR APPLICATION NUMBER: 60/156,634
28     / PRIOR FILING DATE: 1999-09-29
29     / PRIOR APPLICATION NUMBER: 60/156,653
30     / PRIOR FILING DATE: 1999-09-29
31     / PRIOR APPLICATION NUMBER: 60/157,280
32     / PRIOR FILING DATE: 1999-10-01
33     / PRIOR APPLICATION NUMBER: 60/157,294
34     / PRIOR FILING DATE: 1999-10-01
35     / PRIOR APPLICATION NUMBER: 60/157,281
36     / PRIOR FILING DATE: 1999-10-01
37     / PRIOR APPLICATION NUMBER: 60/157,282
38     / PRIOR FILING DATE: 1999-10-01
39     / PRIOR APPLICATION NUMBER: 60/156,633
40     / PRIOR FILING DATE: 1999-09-29
41     / NUMBER OF SEQ ID NOS: 146
42     / SOFTWARE: PatentIn version 3.0
43     / SEQ ID NO 129
44     / LENGTH: 2040
45     / TYPE: DNA
46     / ORGANISM: Homo sapiens
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[illegible]

Db	301	TCGCGCCCTCGAGTGTTCGGGCGCGCTCTGCCCCCTGTCCCTCTTACGTGGGCGAAGGC	360
Qy	1389	TGCACCTACGCCACGCTGTGCACTGACATGACCCGCGCTCAGCGTTCGAGCGCTACCTGGCCATC	1448
Db	361	TGCACCTACGCCACGCTGTGCACTGACATGACCCGCGCTCAGCGTTCGAGCGCTACCTGGCCATC	420
Qy	1449	TGCGCGCCGCTCTCGGCGCCCGCGCTCTTGGTCAACCCGCGCGCGCGTCCGCGCTCATCGCT	1508
Db	421	TGCGCGCCGCTCTCGGCGCCCGCGCTCTTGGTCAACCCGCGCGCGCGTCCGCGCTCATCGCT	480
Qy	1509	GTGCTCTGGGCGGTGAGCGCTGCTCTGCGCGGTCCCTTCTTGTCTCGTGGGCGGTGAG	1568
Db	481	GTGCTCTGGGCGGTGAGCGCTGCTCTGCGCGGTCCCTTCTTGTCTCGTGGGCGGTGAG	540
Qy	1569	CAGGACCCCGGCACTTCGCTAGTCCCGGACCTCAATGCAACCGCGGATGCGCTCTCG	1628
Db	541	CAGGACCCCGGCACTTCGCTAGTCCCGGACCTCAATGCAACCGCGGATGCGCTCTCG	600
Qy	1629	CCTCTGCGCTGTGCGCGCTCTGCGGCTCTGCGGGGCGACACGCGCTCCCGCGCTCG	1688
Db	601	CCTCTGCGCTGTGCGCGCTCTGCGGCTCTGCGGGGCGACACGCGCTCCCGCGCTCG	660
Qy	1689	GCGCCCGAGACCGCGGAGCGCGCGCGCTGTTCACGCGCGAGATGCGGCGAGCCCGCG	1748
Db	661	GCGCCCGAGACCGCGGAGCGCGCGCGCTGTTCACGCGCGAGATGCGGCGAGCCCGCG	720
Qy	1749	CAGCTGGGCGCGCTCGCTGCTAGTGTGGGTGACACCGCGCTACTTCTTCTGCGCTT	1808
Db	721	CAGCTGGGCGCGCTCGCTGCTAGTGTGGGTGACACCGCGCTACTTCTTCTGCGCTT	780
Qy	1809	CTGTGCTCAGCANTCTTACGCGGCTCATTCGCGGCGGAGCTGTGAGCAGCGCGCGCG	1868
Db	781	CTGTGCTCAGCANTCTTACGCGGCTCATTCGCGGCGGAGCTGTGAGCAGCGCGCGCG	840
Qy	1869	CTGCGAGGCGCGGCGCGCTCGGCGCGGAGAGAGGCAACCGCGAGACCTGTGCGTCTG	1928
Db	841	CTGCGAGGCGCGGCGCGCTCGGCGCGGAGAGAGGCAACCGCGAGACCTGTGCGTCTG	900
Qy	1929	CGTAACTGAGACCGCGCGGTGTCCAAAGACGCTGCGTCAAGTCGCGCGCGCGCGAGCT	1988
Db	901	CGTAACTGAGACCGCGCGGTGTCCAAAGACGCTGCGTCAAGTCGCGCGCGCGAGCT	960
Qy	1989	GCGCAACGCTGGGTCCTTCCTTCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCC	2048
Db	961	GCGCAACGCTGGGTCCTTCCTTCCTGCTGCGCCAGCTCTGGGCGCGCTTCCAGCTCC	1020
Qy	2049	--TCCATTTTGATTCACAGCTCCACCGCGCGGTACTTCCATCCCGGAGAAAACATG	2108
Db	1021	TTTCTTATTTGATTCACAGCTCCACCGCGCGGTACTTCCATCCCGGAGAAAACATG	1080
Qy	2107	TCTGTGCCCGAGAGCTCTGGGAGACCCGAGGCGCTTTGAGGGTGGATCCCCGAGTC	2166
Db	1081	TCTGTGCCCGAGAGCTCTGGGAGACCCGAGGCGCTTTGAGGGTGGATCCCCGAGTC	1140
Qy	2167	CGATTCAGTACCAAGCACTGTTTTTCCAGACCTCTGAGACCAAGAGAGAGTTGGTAA	2226
Db	1141	CGATTCAGTACCAAGCACTGTTTTTCCAGACCTCTGAGACCAAGAGAGAGTTGGTAA	1200
Qy	2227	TTCTTAAATCCACACACTGTGATGATGCAAAATGAGAGAGCTCTCAGTGTCTTGAGA	2286
Db	1201	TTCTTAAATCCACACACTGTGATGATGCAAAATGAGAGAGCTCTCAGTGTCTTGAGA	1260
Qy	2287	AGACGAGGAGATTCATTAAGCTAAAAATTTTTTATTAATGTTAAGTATGCTGAAGGC	2346
Db	1261	AGACGAGGAGATTCATTAAGCTAAAAATTTTTTATTAATGTTAAGTATGCTGAAGGC	1320
Qy	2347	TAAAGTAAACCTTGTCTGTATCAAAAATGTAAGTTGTGAGACCTGTGTGAATTTCTT	2406
Db	1321	TAAAGTAAACCTTGTCTGTATCAAAAATGTAAGTTGTGAGACCTGTGTGAATTTCTT	1380
Qy	2407	TTCAACGAGAAACGAAAACCTGTCTCCGAGTGGGTTTGTGAAAGAACCTGCCAAG	2466

Thu Jul 22 08:37:31 2004

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Page 3

Db	1381	TTCAACAGAGAACAGAAAACCTTGCTCCGAAGTGGGTTTGAGAAAGGAAGCCTCCAAAG	1440
Qy	2467	CGGCTGTTCAGAGAAAATGCTCTCTTCGAGTTTATGTCACACCTTGATTAACAATATGGG	2526
Db	1441	CGGCTGTGTGAGAAAATGCTCTCTTCGAGTTTATGTCACACCTTGATTAACAATATGGG	1500
Qy	2527	AGCCTACTATCAGGTTTAAAGCAAGATTCATGACGAGCCTGACGCTGGTCAATTTTCT	2586
Db	1501	AGCCTACTATGCAATTTTAAAGCAAGATTCATGACGAGCCTGACGCTGGTCAATTTTCT	1560
Qy	2587	GGGGTGAAGATCTGCTAGTAGTAAAGTTTCTCTAATTAATTTGCTGTACCTGTATT	2646
Db	1561	GGGGTGAAGATCTGCTAGTAGTAAAGTTTCTCTAATTAATTTGCTGTACCTGTATT	1620
Qy	2647	GCAGATGGTTCCTTGTCGGGGGTGGGGGGGTTATTTGCTCCGCAATGCTTTGGTTAATCCC	2706
Db	1621	GCAGATGGTTCCTTGTCGGGGGTGGGGGGGTTATTTGCTCCGCAATGCTTTGGTTAATCCC	1680
Qy	2707	GGTGTGTGTCTTAATGTTGACAGTGGTGGTGTCTCGCATTTAATTTGCTGGTTGGCC	2766
Db	1681	GGTGTGTGTCTTAATGTTGACAGTGGTGGTGTCTCGCATTTAATTTGCTGGTTGGCC	1740
Qy	2767	TTCCACGTGGCAGAAATCAATTTACATAAACAACGAAAGTTGGCGGATGATGTACTTCTCT	2826
Db	1741	TTCCACGTGGCAGAAATCAATTTACATAAACAACGAAAGTTGGCGGATGATGTACTTCTCT	1800
Qy	2827	CAGTACTTTAACATGTCGCTCGTCCGAACTTTTCTATCTGACCGCATCTATCAACCCAAATC	2886
Db	1801	CAGTACTTTAACATGTCGCTCGTCCGAACTTTTCTATCTGACCGCATCTATCAACCCAAATC	1860
Qy	2887	CTTACAACTCCTCATTTCAAAGAAGTACAGACGGCGGGCCTTTAACTGCTCTCTCGCAAG	2946
Db	1861	CTTACAACTCCTCATTTCAAAGAAGTACAGACGGCGGGCCTTTAACTGCTCTCTCGCAAG	1920
Qy	2947	AAGTCCAGGCGGAGAGGCTTCACAGAAAGCAAGGCACTGCGGGGGAAAGTTGCAAGGGGAC	3006
Db	1921	AAGTCCAGGCGGAGAGGCTTCACAGAAAGCAAGGCACTGCGGGGGAAAGTTGCAAGGGGAC	1980
Qy	3007	ACTGAGAGAGACACGGTGGGCTACACCGGAGCAACGCGCTAACTGTAAAGCAGATGGGATTA	3066
Db	1981	ACTGAGAGAGACACGGTGGGCTACACCGGAGCAACGCGCTAACTGTAAAGCAGATGGGATTA	2040
RESULT 2			
US-10-417-820A-129			
Sequence 129, Application US/10417820A			
Publication No. US20030229216A1			
GENERAL INFORMATION:			
APPLICANT: Chen, Ruoping			
APPLICANT: Liao, Chen W.			
APPLICANT: Lowitz, Kevin			
APPLICANT: Chalmers, Derek T.			
APPLICANT: Behan, Dominic P.			
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled			
FILE REFERENCE: 7 US28.COM			
CURRENT APPLICATION NUMBER: US/10/417,820A			
CURRENT FILING DATE: 2003-04-16			
PRIOR APPLICATION NUMBER: 09/416,760			
PRIOR FILING DATE: 1999-10-12			
PRIOR APPLICATION NUMBER: 09/170,496			
PRIOR FILING DATE: 1998-10-13			
PRIOR APPLICATION NUMBER: 60/110,060			
PRIOR FILING DATE: 1998-11-27			
PRIOR APPLICATION NUMBER: 60/120,416			
PRIOR FILING DATE: 1999-02-16			
PRIOR APPLICATION NUMBER: 60/121,852			
PRIOR FILING DATE: 1999-02-26			
PRIOR APPLICATION NUMBER: 60/109,213			
PRIOR FILING DATE: 1998-11-20			
PRIOR APPLICATION NUMBER: 60/123,944			
PRIOR FILING DATE: 1999-03-12			
PRIOR APPLICATION NUMBER: 60/123,945			

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QY	1929	CGTAAGTGAAG	CGCCCGCTGGTCTCCAAAGACGCTCTGC	CTGCAGTCCGCCCGCGGGAGCC	19888	
Db	901	CGTAAGTGAAG	CGCCCGCTGGTCTCCAAAGACGCTCTGC	CTGCAGTCCGCCCGCGGGAGCC	960	
QY	1989	GGCGAAAGCG	TGGGGTCCCCCTTCCCCGTCCGCCAGCGCTCTGGGGCGCGGCTTCCAGTCC	20438		
Db	961	GGCGAAAGCG	TGGGGTCCCCCTTCCCCGTCCGCCAGCGCTCTGGGGCGCGGCTTCCAGTCC	10220		
QY	2049	--TCC	TATTTGCATTCACACCTCCACCCGCGGTA	CTTCCGATCCCCCGAGAAACATG	21068	
Db	1021	TTTCC	TATTTGCATTCACACCTCCACCCGCGGTA	CTTCCGATCCCCCGAGAAACATG	10888	
QY	2107	TCCGTG	CCCCCAGAGGCTCTGGGGGACCCGAGGGCGCTTGAAGGGTGGGATCCCCGATC	21668		
Db	1081	TCCGTG	CCCCCAGAGGCTCTGGGGGACCCGAGGGCGCTTGAAGGGTGGGATCCCCGATC	11408		
QY	2167	CGATT	CAGTAAACGACAGCTGCTTTTCCAGAGCCTCTGAGAC	CAGAAAGAGTGTGTA	22268	
Db	1141	CGATT	CAGTAAACGACAGCTGCTTTTCCAGAGCCTCTGAGAC	CAGAAAGAGTGTGTA	12008	
QY	2227	TTCTT	TAATCCACCAACCTGGTGAAGTGGCAAAATGAGGAGTCCACAGTGCCTCTGA	22868		
Db	1201	TTCTT	TAATCCACCAACCTGGTGAAGTGGCAAAATGAGGAGTCCACAGTGCCTCTGA	12608		
QY	2287	AGACG	AGGAGATTCATTAAGCTAAATTTTTTATTTATTTATGTAAAGTGAAGTCCAGGC	23468		
Db	1261	AGACG	AGGAGAGATTCATTAAGCTAAATTTTTTATTTATTTATGTAAAGTGAAGTCCAGGC	13208		
QY	2347	TAAAG	TAAACCTGGTCTGATCAAAAGATGAGAGTGCAGACCTGTGTGAATCTT	24068		
Db	1331	TAAAG	TAAACCTGGTCTGATCAAAAGATGAGAGTGCAGACCTGTGTGAATCTT	13808		
QY	2407	TTCAA	CAGAGAACAGAAAACTGTCTCCGAAGTGGGTTTGTGAAGAGACCTGCCAAG	24668		
Db	1381	TTCAA	CAGAGAACAGAAAACTGTCTCCGAAGTGGGTTTGTGAAGAGACCTGCCAAG	14408		
QY	2467	CGGCT	GTGGAGAAATTGCCTCTCGGTTATGTGCACCTGTGATTAACATATGAGG	25268		
Db	1441	CGGCT	GTGGAGAAATTGCCTCTCGGTTATGTGCACCTGTGATTAACATATGAGG	15008		
QY	2527	AGCCT	ACTATGCAAGTTTAAAGCAAGTATCCATGCAAGCTGACAGCTGGTCAATTTTTCT	25868		
Db	1501	AGCCT	ACTATGCAAGTTTAAAGCAAGTATCCATGCAAGCTGACAGCTGGTCAATTTTTCT	15608		
QY	2587	GGGGT	GAGGACTGCTGCTGATGAGAGTTCCTAATTTATTTGGTGTTACTGTGAT	26468		
Db	1561	GGGGT	GAGGACTGCTGCTGATGAGAGTTCCTAATTTATTTGGTGTTACTGTGAT	16208		
QY	2647	GCAAG	TGCTCTGTGCGGGGTATTTTGTCTTCCCAATGCTTTTGTAAATCC	27068		
Db	1621	GCAAG	TGCTCTGTCTGTGCGGGGTATTTTGTCTTCCCAATGCTTTTGTAAATCC	16808		
QY	2707	GGTGT	GTGTATGTTGACAGTGTGGTGGTCTCGGATTAATTAATTTGCTGTGGC	27668		
Db	1681	GGTGT	GTGTGTGTATGTTGACAGTGTGGTGGTCTCGGATTAATTAATTTGCTGTGGC	17408		
QY	2767	TTTCA	CGTTGCAATTAATTAACAGGAAGATTGCGGATGATGTAATCTT	28268		
Db	1741	TTTCA	CGTTGCAATTAATTAATTAACAGGAAGATTGCGGATGATGTAATCTT	18008		
QY	2827	CAGACT	TTAATCATGCTGCTGCAACTTTTCTATCTGAGCGGATCATCAACCATC	28868		
Db	1801	CAGACT	TTAATCATGCTGCTGCAACTTTTCTATCTGAGCGGATCATCAACCATC	18608		
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QY      2947 AAGTTCACGCGCCGAAGAAGCTTTCCAANGAAGCAGGGACA CTGCGGGGGAAAGTTGCAGGGGAC   3086
DB      1921 AAGTTCACGCGCCGAAGAAGCTTTCCAANGAAGCAGGGACA CTGCGGGGGAAAGTTGCAGGGGAC   1980
QY      3007 ACTGAGAGAGACACGCGTGAGGCTTAACCGAGACAAGCGCTTAACGTGAAGCACCATGAGATTA   3066
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RESULT 3
US-10-723-955-129
; Sequence 129, Application US/10723955
; Publication No. US20040110238A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lin, I-Lin
APPLICANT: Liaw, Chen W.
APPLICANT: Lehman-Bruinsma, Karin
APPLICANT: Lowitz, Kevin P.
APPLICANT: Dang, Huang T.
APPLICANT: Chen, Ruoping
APPLICANT: Gore, Martin
APPLICANT: White, Carol
TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
FILE REFERENCE: 7.US29.CON
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US/10/723,955
PRIOR FILING DATE: 2003-4-16
PRIOR APPLICATION NUMBER: 09/416,760
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/1110,060
PRIOR FILING DATE: 1998-11-27
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 60/121,852
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/123,944
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,945
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/123,948
PRIOR FILING DATE: 1999-03-12
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
US-10-723-955-129

Query Match      65.9%; Score 2021.2; DB 17; Length 2040;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2035; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY      1029 ATGGGCAAGCCCCCTGGAAGCGGCAAGCGAGCGGCCCGGAGGGGGCGGAGGCGCGCGTAGGCC   1088
DB      1 ATGGGCAAGCCCCCTGGAAGCGGCAAGCGAGCGGCCCGGAGGGGGCGGAGGCGCGCGTAGGCC   60
QY      1089 GCCTGTCGCGCTTGCAGACGAGCGCGCTGCTCGCCCTTTCCCTGAGGGGCGCTGTCGCG   1148
DB      61 GCCTGTCGCGCTTGCAGACGAGCGCGCGCTGCTCGCCCTTTCCCTGAGGGGCGCTGTCGCG   120
QY      1149 GTGACCGCTGTGTGTGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   1208
DB      121 GTGACCGCTGTGTGTGCTGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   180

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Db 249 TGGCCCTGACCTCTTCCGCTCTGGGAGTACCGGCTTTGGAACTTGGCAACCTGTCTT 308
Qy 1360 GCCGCTGTCCCTCTACGTGGGCGAGGGCTGACCTTACGGCAGCGCTGTCACATGACG 1419
Db 309 GCAAACTCTTCAGTGTCTTGTAGCAGAGCTGCACTTACGCGACAGTGTCTCACCATACCG 368
Qy 1420 CGCTCAGGCTGAGGCGTACTTGGCCATCTGCGCCCGGCTCCGCGCCGCGCTTGTGTCA 1479
Db 369 CGCTGAGGCTGAGGCGTACTTGGCCATCTGCGCCCGGCTCCGCGCCGCGCTTGTGTCA 428
Qy 1480 CCGGCGCGCGGCTCCGCGCGCTATCGCTGTCTGTGGGCGGTGGCGCTGCTCTGTCCG 1539
Db 429 CCAAGGGCGCGGTAAAGGTGGTATCTCGTCACTTGGGCGGTGGCGCTTGTGAGGCGCG 488
Qy 1540 GTCCCTTCTGTCTCTGTGTGGGCTCGAGCAGAGACCCCGCA 1581
Db 489 GGCCCATCTTGTGTGTGTGGTGGAGTGGAGCATGATTAACGGCA 530

RESULT 10
US-10-303-204A-4
; Sequence 4, Application US/10303204A
; Publication No. US2003016514A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris P.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberatori, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1029
; TYPE: DNA
; ORGANISM: sus scrofa
US-10-303-204A-4

Query Match 7.5%; Score 230; DB 15; Length 1029;
Best Local Similarity 68.6%; Pred. No. 4.2e-45;
Matches 317; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
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Db 266 CGCTCTTCCACCCGCTGTGGCGGCTGACCGCACTTCCGCGGCTTCTGTGTG 325
Qy 1180 TCGGGGTGAGCGGAGCGTGTGACCGTGTGATGCTGATCGGGGCTTACCGGAGCATGCGGA 1239
Db 326 TGGGTATCGGGGAGCACTGTCTGACGATGCTGTAGTGTACCGCTTCCGCGAGATGCGCA 385
Qy 1240 CCACCCAACTGTACTGTGAGGAGCATGCGCGCTGTCCGACCTTACTGTACTGTGCGGC 1299
Db 386 CCACCCAACTGTACTGTGAGGAGCATGCGCGCTTCCGACCTTACTGTACTGTGCGCA 445
Qy 1300 TGGCGTTCGACCTGTACCGGCTCTGGGCGCTCGGGGCGCTGGGGTGTGGGCGCGCTGTCT 1359
Db 446 TGGCCCTTCGACTCTTCCGCTTGTGGCAGTACCGGCGCTTGGAACTTGGCAACTGTCTCT 505

Qy 1360 GCCGCTGTCCCTCTACGTGGGCGAGGGCTGCACTTACGCCAGCGCTGTGCAATGACCG 1419
Db 506 GCAAACTCTTCAGTGTCTTGTAGCAGAGCTGCACTTACGCGACAGTGTCTCACCATACCG 565
Qy 1420 CGCTCAGGCTGAGGCGTACTTGGCCATCTGCGCCCGGCTCCGCGCCGCGCTTGTGTCA 1479
Db 566 CGCTGAGGCTGAGGCGTACTTGGCCATCTGCGCCCGGCTCCGCGCCGCGCTTGTGTCA 625
Qy 1480 CCGGCGCGCGGCTCCGCGCGCTATCGCTGTGTGTGGGCGGTGGCGCTGCTCTGTCCG 1539
Db 626 CCAAGGGCGCGGTAAAGGTGGTATCTCGTCACTTGGGCGGTGGCGCTTGTGAGGCGCG 685
Qy 1540 GTCCCTTCTGTCTCTGTGTGGGCTCGAGCAGAGACCCCGCA 1581
Db 686 GGCCCATCTTGTGTGTGTGGTGGAGTGGAGCATGATTAACGGCA 727

RESULT 11
US-10-305-720-359
; Sequence 359, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Yang, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 359
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inycle ID No. US20040010136A1 2018536
; NAME/KEY: unsure
; LOCATION: (1) ... (250)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-359

Query Match 7.5%; Score 229; DB 16; Length 250;
Best Local Similarity 98.8%; Pred. No. 4.3e-45;
Matches 240; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Db 1 TCTCAGTACTTAACTGCTGCTGCTGCACTTTCTTATCTGAGCGCTTATCAACCCA 60
Qy 2884 ATCTCTTCAACCTTCTTCAAGAGTACGAGCGCGCTTAACTGTGCTGTGCA 2943
Db 61 ATCTCTTCAACCTTCTTCAAGAGTACGAGCGCGCTTAACTGTGCTGTGCA 120
Qy 2944 AGAAGTTCAGGCGGAGAGGCTTCCACAGAGGAGCACTGTGGGGGAAATTGCGAGG 3003
Db 121 AGAAGTTCAGGCGGAGAGG-TTCCACAGAGGAGGAGCACTGTGGGGGAAATTGCGAGG 179
Qy 3004 GACACTGAGAGAGACAGGTGGGCTACACCGAGAGCAAGCCCTAAGCTGAAGAGATGCGGA 3063
Db 180 GACACTGAGAGAGACAGGTGGGCTACACCGAGAGCAAGCCCTAAGCTGAAGAGATGCGGA 239
Qy 3064 TAA 3066
Db 240 TAA 242

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US-10-225-567A-139
; Sequence 139, Application US/10225567A
; Publication No. US20030113798A1


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Db      840 CGAGTGGCGCCGCCACCGAGTTTGGCGTGGAGCTGCTCAAGGTATGGTGGG 899
Qy      1660 CGCGGGGCGCCACCGCCGTCGCGGGGCGCCGAGACCGGAGAGCGCGCGCTGT 1719
Db      900 GTCCAGGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 959
Qy      1720 TCAGCCCGGAATGCGGCGCCGAGCCCGCGCAGCTGGGCGCGCTGTCATGCTGG 1779
Db      960 CAGGAAGCTGTGGCGGAGAGCGCGCGAGTGTGTGGTGGCTCGCTCAGGAGCA 1019
Qy      1780 TCACCAAGCGCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1839
Db      1020 GACCAACAAGCAACCGTGAATAATGCTGGTGGTCTCAGCGCGCTTCTTCTTCT 1079
Qy      1840 GCGCGGAGCTGT 1851
Db      1080 CGCGGCTCTAT 1091
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RESULT 14
US-10-303-204A-15
; Sequence 15, Application US/10303204A
; Publication No. US2003016614A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: rattus norvegicus
US-10-303-204A-15
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Best Local Similarity 68.4%; Pred. No. 1.1e-44;
Matches 316; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy      1120 CGCCCTTCCCTGGGGGCGCTGTGCGGTGACCGCTGTGCTGCTGCTGCTGCTG 1179
Db      104 CGCTGTCCCGCTCGCTGCTGCGAGGCTGACCGGACCTGCGTGGGCGCTTGTGG 163
Qy      1180 TCGGGGTGAGCGGCAAGTGTGACCGTGTATGCTGATCGGGCGCTACCGGAGATCGGA 1239
Db      164 TGGGCACTTCAGGAACTCTCACTATGCTGTGGTGTGCTCCGCTTCCGAGAGCTGGCA 223
Qy      1240 CCAACCAACTTGTACTGTGGGAGCATGAGCGCTGTCCGACTACTCATCTGCTGCGGC 1299
Db      224 CCAACCAACTTGTACTGTGCAAGATGAGCGCTTCTGAGATGCTGCTCATCTTCTGTGA 283
Qy      1300 TGGCGTTGACCTGTACCGCTCTGCGGCTGCGGCGCTGGGTGTTGGAGCGCTGCTCT 1359
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Qy      1420 CGCTCAGGCTGAGAGCTTACTGTCATCTGCGCGCGCTGCTGCGCGCGCTGCTGCTGCTG 1479
Db      404 CGCTGAGGTGAGAGCTTACTGTCATCTGCGCGCGCTGCTGCGCGCGCTGCTGCTGCTG 463
Qy      1480 CCGCGCGCGCGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1539
Db      464 CTAAGGCGCGCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 523
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RESULT 15
US-10-303-204A-14
; Sequence 14, Application US/10303204A
; Publication No. US2003016614A1
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.
; APPLICANT: Van Der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: GROWTH HORMONE SECRETAGOGUE RECEPTOR
; TITLE OF INVENTION: FAMILY
; FILE REFERENCE: 19589PCA
; CURRENT APPLICATION NUMBER: US/10/303,204A
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 09/077,674
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US96/19445
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: 60/018,962
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 60/008,582
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 3129
; TYPE: DNA
; ORGANISM: rattus norvegicus
US-10-303-204A-14
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Best Local Similarity 68.4%; Pred. No. 1.1e-44;
Matches 316; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy      1120 CGCCCTTCCCTGGGGGCGCTGTGCGGTGACCGCTGTGCTGCTGCTGCTGCTGCTG 1179
Db      104 CGCTGTCCCGCTCGCTGCTGCGAGGCTGACCGGACCTGCGTGGGCGCTTGTGG 163
Qy      1180 TCGGGGTGAGCGGCAAGTGTGACCGTGTATGCTGATCGGGCGCTACCGGAGATCGGA 1239
Db      164 TGGGCACTTCAGGAACTCTCACTATGCTGTGGTGTGCTCCGCTTCCGAGAGCTGGCA 223
Qy      1240 CCAACCAACTTGTACTGTGGGAGCATGAGCGCTGTCCGACTACTCATCTGCTGCGGC 1299
Db      224 CCAACCAACTTGTACTGTGCAAGATGAGCGCTTCTGAGATGCTGCTCATCTTCTGTGA 283
Qy      1300 TGGCGTTGACCTGTACCGCTCTGCGGCTGCGGCGCTGGGTGTTGGAGCGCTGCTCT 1359
Db      284 TGGCGGTGACCTGTGCTGCTGCTGCGGAGTACCGGCGCTGGAACTTGGCGACCTGCTCT 343
Qy      1360 GCCCGCTGCTCCCTGACGTGGGCGAGGCTGACACTTACGCCACGCTGCTGACATGACCG 1419
Db      344 GCAAACTTTCAGATTGTTCAGCAGAGAGCTGACACTTACGCCACGCTGCTGACATGACCG 403
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QY 1420 CGCTCAGCGTCGAGCGGCTACCTGCGCATCTGCGCGCCGCTCCGCGCCCGCGTCTTGATCA 1479
 Db 404 CGCTGAGCGTCGAGCGGCTACCTGCGCATCTGCTTCCTCTGCGGCGCCAGGTGATCA 463
 QY 1480 CCGGCGCGCGCGGTCGCGCGCTCATCGCTGCTCTGCGCGCGTGGCGCTGCTCTGCGG 1539
 Db 464 CTAGGCGCGCGGTGAAGCTGATCTCTGTCATCTGCGCGCGTGGCTTTCTGACGCGG 523
 QY 1540 GTCCCTTCTTGTCTCTGCTGCGCGCTGACGAGAGACCCGCGCA 1581
 Db 524 GCGCCATCTTCTGCTGCTGCGCGCTGAGCAGAGAAACGCGCA 565

Search completed: July 17, 2004, 23:55:39
 Job time : 1295 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 17, 2004, 16:22:38 ; Search time 7448 Seconds

(Without alignments)
12292.850 Million cell updates/sec

Title: US-09-719-485-1

Perfect score: 3066

Sequence: 1 ttgaattactctgtctacatg.....acgtgaagacgatgggataa 3066

Scoring table: IDENTITY_NUC

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estb1:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estrov:
6: em_estrpl:
7: em_estro:
8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_esthum:
16: em_estom:
17: em_gss_hum:
18: em_gss_hiv:
19: em_gss_pln:
20: em_gss_vrl:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rtd:
26: em_gss_phg:
27: em_gss_vrl:
28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693.8	22.6	843	13	BUS53576
2	576	18.8	850	10	BFS13101
3	490.2	16.0	495	10	BFS12085
4	360.6	11.8	399	28	AQ939773
					AQ939773 NR5-116R

5	255.8	8.3	425	28	AQ138681	HS_3073_A
6	231.6	7.6	1046	29	AY407666	Mus muscu
7	230	7.5	4435	11	AK049671	Mus muscu
8	227.8	7.4	1052	29	AY407664	Homo sapi
9	226.8	7.4	500	13	BF603623	269181 MA
10	219.2	7.1	608	13	BY724644	BY724644
11	213.2	7.0	969	29	AY407665	Par trogl
12	204	6.7	370	13	EX485214	EX485214
13	200.8	6.5	489	9	AL042230	DKFZP686
14	198.2	6.5	2669	11	BC035179	BC035179
15	197.8	6.5	606	13	BO778458	BO778458
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17	197.8	6.5	712	14	CD364687	CD364687
18	197.8	6.5	721	14	CD364665	CD364665
19	197.8	6.5	779	14	CA442904	CA442904
20	197.2	6.4	982	13	EX370686	EX370686
21	196.8	6.4	639	12	BM992802	BM992802
22	196.2	6.4	391	9	AI569401	AI569401
23	196.2	6.4	656	14	CA420015	CA420015
24	196	6.4	741	29	AG113248	AG113248
25	195.2	6.4	337	13	BUS66980	BUS66980
26	194.8	6.4	457	10	BF939646	BF939646
27	193.6	6.3	416	14	CD520893	CD520893
28	193.4	6.3	353	9	AV657198	AV657198
29	193.4	6.3	854	28	AQ747659	AQ747659
30	193	6.3	537	28	AQ122719	AQ122719
31	193	6.3	739	28	AQ35003	AQ35003
32	192.6	6.3	486	12	BG331842	BG331842
33	192.6	6.3	624	14	CA423118	CA423118
34	192.6	6.3	691	14	CD243422	CD243422
35	192.6	6.3	953	12	BI084622	BI084622
36	192.4	6.3	680	12	BM990843	BM990843
37	192.2	6.3	663	9	AV703573	AV703573
38	192	6.3	546	9	AI889995	AI889995
39	192	6.3	699	28	AQ389756	AQ389756
40	191.4	6.2	365	14	CD688147	CD688147
41	191.4	6.2	447	13	EX489032	EX489032
42	191.2	6.2	2546	11	BC027960	BC027960
43	191	6.2	462	9	AI924207	AI924207
44	191	6.2	538	9	AU143917	AU143917
45	191	6.2	556	13	BQ183587	BQ183587

ALIGNMENTS

RESULT 1
BUS53576 843 bp mRNA EST 16-SEP-2002
LOCUS
DEFINITION AGENCOURT 10242213 NIH MGC 109 Homo sapiens cDNA clone
IMAGE:6577973 5', mRNA sequence.
ACCESSION BUS53576
VERSION BUS53576.1 GI:229303848
KEYWORDS
SOURCE
ORGANISM
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
NIH-MGC <http://mgc.ncl.nih.gov/>
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L10M2778 row: P column: 05
High quality sequence stop: 534.

Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_SEQ=None found"

ORIGIN

Query Match 18.8%; Score 576; DB 10; Length 590;
Best Local Similarity 99.7%; Pred. No. 1.9e-55;
Matches 588; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

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DB 1 CGGCGCGTGGAGAGCGCGCGCGCTCGGGGGGAGAGAGCCGCGAGACCGTCCG 60
QY 1923 GTCTGTGAGTGGAGAGCGCGCGCGTCCGAGAGCGCGTCCGAGTCCGCGCGCG 1982
DB 61 GTCTGTGAGTGGAGAGCGCGCGCGTCCGAGAGCGCGTCCGAGTCCGCGCGCG 120
QY 1983 GGGAGCGCGAGAGCGTGGGTCCTTCCCTGCTCGGCCAGCTCTGGGGCGCGCTTCCA 2042
DB 121 GGGAGCGCGAGAGCGTGGGTCCTTCCCTGCTCGGCCAGCTCTGGGGCGCGCTTCCA 180
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QY 2281 TTGAGAAACAGAGGAGATTTCACTAAATTTTATTTATTTAATGTTAAGTACT 2340
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QY 2341 GAAAGCTAAAGTAAACCTTGTCTGATCAAAAGTAAAGTATGTCAGACCTGTGTAGA 2400
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RESULT 2
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LOCUS UI-H-BM1-ami-e-11-0-UI.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone
IMAGE:3070172 3', mRNA sequence.

ACCESSION BFS12085
VERSION BFS12085.1 GI:11597297

KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 495)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
01190-df track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA library preparation: M.B.
Soares lab clone distribution: NCI-CGAP clone library distribution
Information can be found through the I.M.A.G.E.S. Consortium/ILM at:

FEATURES

source

www.bio.lnlnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 190-253.
>GC_rich#Low complexity
Seq primer: M13 Forward
POLYA=No.

Location/Qualifiers
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polylinker. Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub7
is a subtracted library derived from NCI CGAP Sub6. The
NCI CGAP Sub7 library had 12 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub6 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kid5 pool 1 LLM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones 1323912-1325831, 1471368-1472903, 3578-3582,
1492104-1493255); NCI CGAP Lys pool 1 LLM 3578-3582,
3851-3854 (IMAGE Clones 1414920-1417991,
1520904-1522439); NCI CGAP GC4 pool 1 LLM 3164-3167,
3716-3720, 3733-3735 (IMAGE Clones
1257096-1258631, 1469064-1470983, 1475592-1476743);
NCI CGAP Pr22 pool 1 LLM 2457-2459, 2758-2759, 3062-3068
(IMAGE Clones 985608-986759, 1101192-1101959,
1217928-1220615); NCI CGAP Co10 pool 1 LLM 2644-2653,
2871-2872 (IMAGE Clones
1057416-1061255, 1144584-1145351). (6% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI CGAP Sub1 (IMAGE Clones 2708616-2710535) and
NCI CGAP Sub2 (IMAGE Clones 2710536-2712455) (4% of
the driver population), plus a pool of 11,136 clones from
NCI CGAP Sub3 (IMAGE Clones 271456-2723591) (10% of
the driver population), plus a pool of 5,472 clones from
NCI CGAP Sub4 (IMAGE Clones 2723592-2728326) (40% of the
driver population), plus a pool of 4032 clones from
NCI CGAP Sub6 (IMAGE Clones 2728969-2731190) (40% of the
driver population). Subtraction was performed as
previously described (Bonaldi, Lemmon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_SEQ=None found"

ORIGIN

Query Match 16.0%; Score 490.2; DB 10; Length 495;
Best Local Similarity 99.4%; Pred. No. 3.5e-49;
Matches 492; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 582 CCAGACCAATCCCTTGAAGTCCCGGAGTACCACTGACAAAGCGCCGTACACT 641
DB 435 CCAGACCAATCCCTTGAAGTCCCGGAGTACCACTGACAAAGCGCCGTACACT 376
QY 642 GCTCAGTCCGTAAACAAAGCTGTAGAGGTGACAGATCGTCCACCGGAGCGGAGAGG 701
DB 375 GCTCAGTCCGTAAACAAAGCTGTAGAGGTGACAGATCGTCCACCGGAGCGGAGAGG 316
QY 702 CTGTCGCTTAAGGCGCGGCTATTCAGTTAGTGAAGGAGAAAGCGCCGTGAACCTGC 761
DB 315 CTGTCGCTTAAGGCGCGGCTATTCAGTTAGTGAAGGAGAAAGCGCCGTGAACCTGC 256
QY 762 ATGGGCGCGGAGAGGCGCGGAGCGAGATGCGCGGCGCGGCGCGGCGCGT 821
DB 255 ATGGGCGCGGAGAGGCGCGGAGCGAGATGCGCGGCGCGGCGCGGCGCGT 196
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 QY 882 TCTGCGCGCGCGCGAGCGCGAGCGCGCTCCGCGCTGACCTGCGCGCGCGCGAGCGTG 941
 Db 135 TCTGCGCGCGCGCGAGCGCGAGCGCGCTCCGCGCTGACCTGCGCGCGCGCGAGCGTG 76
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 ACCESSION A0939773
 VERSION A0939773.1 GI:7216151
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 399)
 AUTHORS Zabarovsky, E.R., Gzatalullin, R., Podowski, R.M., Zabarovska, V.V.,
 Xie, L., Muravenko, O.V., Kozlov, S., Petrenko, L., Skobelev, N.,
 Li, J., Protodopov, A., Kashuba, V., Ernberg, I., Winberg, G. and
 Wahlstedt, C.
 TITLE NotI clones in the analysis of the human genome
 JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
 MEDLINE 20175728
 PUBMED 10710430
 COMMENT Contact: Podowski RM
 Center for Genomics Research
 Karolinska Institute
 17177 Stockholm, Sweden
 Tel: +46-8-728-6372
 Fax: +46-8-337983
 Email: Raf.Podowski@cgr.ki.se
 Class: NotI site.
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 Best Local Similarity 96.2%; Pred. No. 1.1e-33;
 Matches 380; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
 QY 624 CAAAAGCGCCGTAACAGTGTCTGCTGTAACCAAGCTGTAGAGTGCAGACATCCG 683
 Db 395 CAAAAGCGCCGTAACAGTGTCTGCTGTAACCAAGCTGTAGAGTGCAGACATCCG 336
 QY 684 TCACCGGACCGGGTACGGCTCGCGCTAGAGCGCGCGGTA-TTCAGTTAGTGAGAG 742
 Db 335 TCACCGGACCGGGTACGGCTCGCGCTAGAGCGCGCGGTA-TTCAGTTAGTGAGAG 276
 QY 743 GGAAGCGCCGTAACAGTGTCTGCTGTAACCAAGCTGTAGAGTGCAGACATCCG 802
 Db 275 GGAAGCGCCGTAACAGTGTCTGCTGTAACCAAGCTGTAGAGTGCAGACATCCG 216
 QY 803 CGGGGCGGCGCGCGCGCGCGGAGACTGCGCGCACTGCTCGGAGCGCGCTTGAGAG 862

Db 215 CGGGGCGGCGCGCGCGCGCGCGGAGACTTGGCGGCGCACTGCTCGGAGCGCGCTTGAGAG 156
 QY 863 CCACCGCGGAGAGCGCGCTTCTCGCGCGCGCGAGCGAGCGCGAGCGCGCTTGAGAG 922
 Db 155 CCACCGCGGAGAGCGCGCTTCTCGCGCGCGCGAGCGAGCGCGAGCGCGCTTGAGAG 96
 QY 923 CTGCGCGCGCGCGAGCGCGCGCGCTGCGGAGAGCGCGCTTACCGAGAGGAGACCGCGC 982
 Db 95 CTGCGCGCGCGCGAGCGCGCGCGCTGCGGAGAGCGCGCTTACCGAGAGGAGACCGCGC 36
 QY 983 CAGGCTCCAGCGCGCGCGCGGAGCGCGCGCGCGC 1017
 Db 35 CAGGCTCCAGCGCGCGCGCGGAGCGCGCGCGCGC 1
 RESULT 5
 A0138681 425 bp DNA linear GSS 24-SEP-1998
 LOCUS HS 3073 A2 D02 MR CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=3073 Col=4 Row=G, genomic survey
 sequence.
 ACCESSION A0138681
 VERSION A0138681.1 GI:3529334
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 425)
 AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3073 row: G column: 4
 Class: BAC ends
 High quality sequence stop: 425.
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 source 1..425
 location/Qualifiers
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 E-Coli DH10B"
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 Best Local Similarity 94.2%; Pred. No. 3.2e-21;
 Matches 274; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
 QY 2397 TAGAATTTTTCACAGAGAGAGAACTTGTCTCGAAGTGGGTTGTGAGAGAG 2456
 Db 51 TCGAATTTTTCACAGAGAGAGAACTTGTCTCGAAGTGGGTTGTGAGAGAG 110
 QY 2457 CCTGCGAAGGCGCGCTTGTTCAGAGAAATGCTCTTGTGTTATGTCAGCCTTGATA 2516
 Db 111 CCTGCGAAGGCGCGCTTGTTCAGAGAAATGCTCTTGTGTTATGTCAGCCTTGATA 170
 QY 2517 CACATATGAGAGCCTTACTATGACGTTTAAAGCAAGATATCATGACGCTTGACGCTGT 2576

Db	171																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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Db 179 CACACCACTCTACCTGTCCAGCATGGCCTTCTCCGATGTGCTCATCTTCCCTGCAT 238
 QY 1301 GCCGTGACCTGTACCGCCTCTG3CGCTCGCGGCCCTGGGTGTTCGGGCGGCTGCTTG 1360
 Db 229 GCCCTGGACCTCGTGGCCCTCTG3CAGTACCGGCCCTGGAACTTCGCGACCTCCCTTG 298
 QY 1361 CCGCGTGCCTCTACGAGGCGAGGGGTGCACCTAGCCACGCGTGTGCACATGACCG 1420
 Db 299 CAACTCTTCCATTCGTAGTAGAGCTGACCTTAGCCACGAGTGTCTACCATCAACG 358
 QY 1421 GCTGAGCGTGAAGCGCTACCTGCGCATCTGCGGCCGCTCGCGCGCGCTTGTGTAC 1480
 Db 359 GCTGAGCGTGAAGCGCTACCTGCGCATCTGCGGCCGCTCGCGCGCGCTTGTGTAC 418
 QY 1481 CCGGCGCGCGCTCGCGCGCTCATCGCTGTGCTGTGGCGCGTGGCGGCTGTGCGCG 1540
 Db 419 CAAAGGCGCGGTGAAGCTGTGATCTTCTCATCTGGGCGCTGCGCTTGTGACGCGCG 478
 QY 1541 TCCCTTCTTCTCTGCTGCGCGCTGAGCAGACCGCGGCATC 1583
 Db 479 GCCCATCTTCTGCTGCTGCGGCGTGGAGCAGACGAGCGCAC 521

RESULT 9

BF603623

LOCUS 269181 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION

BF603623.1 GI:11701421

KEYWORDS

SOURCE

ORGANISM

Bos taurus

Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 500)

Smith,T.P.L., Groves,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,

Caesa,E., Wray,J.B., White,J., Cho,U., Fahnensterg,S.C.,

Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,

Chitko-McKown,C.G., Pettea,G., Holt,I., Karanycheva,S., Liang,F.,

Quackenbush,J. and Keise,J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

11282978

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt. trimmed with phred

v0.980904.e. Vector identified by cross_match with the -mismatches

and -mismatch 12 options.

PCR primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCAGCTACGACGACG

Plate: 49

row: 1

column: 6

Seq primer: ATTAGGTGACATGATG.

Location/Qualifiers

1..500

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/mol_type="RNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 3BOV"

/note="Vector: pCMV SPOR6; Site 1: NotI; Site 2: SalI;

library made from pooled tissue from marrow, alveolar

macrophage, ovary, fetal semitendinosus muscle, and fetal

longissimus muscle."

ORIGIN

Query Match 7.4%; Score 226.8; DB 10; Length 500;
 Best Local Similarity 68.2%; Pred. No. 8,-18;
 Matches 315; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 1120 CCGCCTTTCCTGGGCGCGCTGTGCGCGGTACCGCTGTGTGCTGTGCTGTGCTGTG 1179
 Db 39 CCGCTTCCCGCGCGCGCTGTGCGCGGTACCGCTGTGTGCTGTGCTGTGCTGTG 98
 QY 1180 TCGGGGTGAGCGGCAAGTGTGACCGGTATCTGTATCGGGGCTTACCGGCAATGCGGA 1239
 Db 99 TGGGCAATCGCGGCAACCTGTACACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 158
 QY 1240 CCACACCAACTTGTACCTGTGCGAGATGGCGGTGTGCGACCTTACATCTGTGTGCGGC 1299
 Db 159 CCACACCAACTTGTACCTGTGCGAGATGGCGGTGTGCGACCTTACATCTGTGTGCGGC 218
 QY 1300 TGGCGTGTGACCTGTACCGCTGTGCGCGCTGTGCGCGCTGTGCGCGCTGTGCT 1359
 Db 219 TGGCGTGTGACCTGTACCGCTGTGCGCGCTGTGCGCGCTGTGCGCGCTGTGCT 278
 QY 1360 GCGCGCTGTGCTGTACCGCTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGT 1419
 Db 279 GCAACTCTTCCAGTGTGTGCGAGAGTGTGCGAGTGTGCGAGTGTGCGAGTGTGCGAGT 338
 QY 1420 CCGTCAAGCTGTGAGCGCTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGT 1479
 Db 339 CCGTCAAGCTGTGAGCGCTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGT 398
 QY 1480 CCGCGCGCGCGCGCTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCG 1539
 Db 399 CCAAGGCGCGGCGTGAAGCTGTGATCTGTGATCTGTGATCTGTGATCTGTGATCTGTG 458
 QY 1540 GTCCCTTCTTCTCTGCTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCGGTGTGCGCG 1581
 Db 459 GCCCATCTTCTGCTGTGCTGTGCGAGTGTGAGACATGAGATGCA 500

RESULT 10

BY724644

LOCUS

DEFINITION

BY724644 RIKEN full-length enriched, 0 day neonate thymus Mus

608 bp mRNA linear EST 17-DEC-2002

BY724644

BY724644.1 GI:27137769

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 608)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondou,S.,

Nikado,I., Osato,N., Saito,R., Suzuki,H., Yamazaki,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,I.,

Schonbach,C., Gotohori,T., Baldarelli,R., Hill,D.P., Bull,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,

Chotia,C., Corbani,L.S., Cousins,S., Dalia,B., Dragan,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gutholdi,M., Gissi,C., Godzik,A., Gough,J., Griffland,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lemhard,B., Lyons,P.A., Maglott,D.R.,

Matsais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okado,T., Pavani,W.U., Ferreira,G., Fesole,G.,

Petrovsky,N., Pillai,R., Pontius,U.V., Qi,D., Ramachandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Santelin,A., Schneider,C., Sempile,C.A., Setou,M., Shindada,K.,

Sultana,R., Takekawa,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilting,L.G., Wynshaw-Boris,A., Yangisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,N., Zhu,Y., Zimmer,A., Zimmet,P.,

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location/Qualifiers
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/organism="Mus musculus"
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/tissue_type="thymus"
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/lab_host="DH10B"
/clone_id="RIKEN full-length enriched, 0 day neonate
thymus"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'.
GAGGAGAGAGAGATCCAGAGCGCTTTTCTTTTCTTTTNN 3']. cDNA was
prepared by using tetraose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGGAGAGAGATTCGAGTTATTTAAATTATCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified Bluescript KS(+) after bulk excision from Lambda

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ORIGIN	FLC I."
Query Match	7.1%; Score 219.2; DB 13; Length 608;
Best Local Similarity	70.3%; Pred. No. 6.6e-17;
Matches 293; Conservative	0; Mismatches 124; Indels 0; Caps 0;
OY	1165 TGTGCGCTTGCTGTGTGGGGGTGAGCGGGCAACGTGTGACCGGTGATCTGATCGGGGCT 1224
Db	2 TGGCGCTCTTGATGTGTGGGCACTCTCGGGCAACCTGTGCACCATGCTGTGTGTGTCCCGCT 61
OY	1225 ACCGGGACATGCGGACCAACCACTTGTACTGTGGGACATAGCCGTGTCCGACCTAC 1284
Db	62 TCGCGGAGCTGGGACCAACCACTTGTACTGTGGGACATAGCCGTGTCCGACCTAC 121
OY	1285 TCATCTTGCTGGGCTCCGTTGACTGTACCGCTCTTGGCGCTCGCGGCTGTGGGT 1344
Db	122 TCATCTTGCTGGGATCCGCTGACCTGTCCGCTCTGACGTATCGGCGCTGTGAACT 181
OY	1345 TCGGGGCGCTGTCTGCGCGCTGTCCCTTACGTGGGCGAGGCTGCACCTACGCCACG 1404
Db	182 TCGCGGACCTGCTGTGAACTCTTCCAGTTTGTACGAGAGACTGCACCTACGCCACG 241
OY	1405 TGTGCACATGACCGCGCTGACGCTGACGCGCTACCTGTGCGCATCTGCGCGCTCCG 1464
Db	242 TCCCTACCATCACCGCGCTGAGCGCTGACGCGCTACCTGTGCGCATCTGCTCCGCTGGG 301
OY	1465 CCGCGCTGTGTGTACCCGCGCGCGCTCGCGCGCTCATCGCTGTGTGGGCGGTG 1524
Db	302 CCAAGGTGTGTGTACCAAGGCGGTGTGAAGCTGTGTCTGTGTCTGTGTGTGTGTGTGT 361
OY	1525 CGCTGCTCTGTGCGCGCTTCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1581
Db	362 CTTCTGACACCGCGCGCGCGCTCATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 418
RESULT 11	
LOCUS	AY407665
DEFINITION	Pan troglodytes GHR gene, VIRUAL TRANSCRIPT, partial sequence,
ACCESSION	AY407665
VERSION	AY407665.1
KEYWORDS	GT:39763636
SOURCE	GSS.
ORGANISM	Pan troglodytes (chimpanzee)
REFERENCE	1 (bases 1 to 969)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PubMed	14671302
REFERENCE	2 (bases 1 to 969)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
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ORIGIN

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Query Match 6.5%; Score 200.8; DB 9; Length 489;
Best Local Similarity 77.9%; Pred. No. 1.1e-14;
Matches 268; Conservative 0; Mismatches 72; Indels 4; Gaps 2;

QY 2 TGAATATCTGTCACCTGCGCGCGGCTGCTACGCTGTAATCCAGCACTTTGGG 61
DB 147 TGAATATCTGTCACCTGCGCGCGGCTGCTACGCTGTAATCCAGCACTTTGGG 206
QY 62 AGGTGAGCGCGGTGACCACTGGGCTCAGAGTTTGAGACCAAGCTGGCCAACTGGC 121
DB 207 AAGCGAGGCGAGGTGATCCTGAGGTGAGAGTTTGAGACCAAGCTGGCCAACTGGT 266
QY 122 GAACCCCTGACTACCAAAAAACAATAATTAGCCGCGGCTTTGGG---GCTCTGTGC 178
DB 267 GAACCCCGCTTTACTTAACCTCAAAAAATTAGCTGGGCGTGTGCAAGGCACTTGTGA 326
QY 179 TCCAGCTACTCAGAGGCTGAGGTGGAGAGCTTTGAGCTTGGAGGTCGAGGCTGC 238
DB 327 TCCAGCTACTCAGAGGCTGAGGCGAGAGATTGCTTGGCCCTGGAGGTGAGGCTTGC 386
QY 239 AGTGAAGTGTATCGCGCACTTAACCTCCAGCTGAGACGACAGTGAAGACCTGTCAA 298
DB 387 AGTGAAGCAATGCTCTCA--TTGCATCTCCAGCTTGGGTGACAGTGAATCTCATCTCAA 445
QY 299 GAAGAAAAAAGAAAGAAAGAAAGAAAAAAGAAAAAAGAA 342
DB 446 AATTAAGATTAAGATATGTCTCAAAAAAAGAAAAA 489

RESULT 14
BC035179 2669 bp mRNA linear HTC 04-MAR-2003
LOCUS Homo sapiens, clone IMAGE:5266192, mRNA.
ACCESSION BC035179
VERSION BC035179.1 GI:23273366
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2669)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshlyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadnesystemsbiology.org
Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Series: IRAK Plate: 73 Row: o Column: 3
This clone has the following problem: retained intron.

FEATURES

source 1.2669
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:5266192"
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ORIGIN

Query Match 6.5%; Score 198.2; DB 11; Length 2669;
Best Local Similarity 68.2%; Pred. No. 1.2e-14;
Matches 305; Conservative 0; Mismatches 138; Indels 4; Gaps 2;

QY 2 TGAATATCTGTCACCTGCGCGCGGCTGCTACGCTGTAATCCAGCACTTTGGG 61
DB 1252 TGAAGGAATGAAACAGCTGGGCGCAGTGGCTCAAGCTGTAATCCAGCACTTTGGG 1311
QY 62 AGGTGAGCGCGGTGACCACTGGGCTCAGAGTTTGAGACCAAGCTGGCCAACTGGC 121
DB 1312 AAGCTGAGCGGATGATGATCCTGAGGTGAGAGTTTGAGACCAAGCTGGCCAACTGGT 1371
QY 122 GAACCCCTGACTACCAAAAAACAATAATTAGCCGCGG---GCTTGGCGCTTCTGTGC 178
DB 1372 GAACCCCGCTTTACTTAACCTCAAAAAATTAGCTGGGCGTGTGCAAGGCACTTGTGA 1431
QY 179 TCCAGCTACTCAGAGGCTGAGGTGGAGAGCTTTGAGCTTGGAGGTCGAGGCTGC 238
DB 1432 TCCAGCTACTCAGAGGCTGAGGCGAGAGATTGCTGGAACCTGGAGGTGAGGCTGC 1491
QY 239 AGTGAAGTGTATCGCGCACTTAACCTCCAGCTGAGACGACAGTGAAGACCTGTCAA 298
DB 1492 AGTGAAGCAATGCTCTCA--TTGCATCTCCAGCTTGGGTGACAGTGAATCTCATCTCAA 1550
QY 299 GAAGAAAAAAGAAAGAAAGAAAGAAAAAAGAAAAAAGAAATTTGGTCAATTAT 358
DB 1551 AAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAAAAGAAAAAAGAAATAGAAC 1610
QY 359 ATGTCAGCTCCCTCCACACTCGGAATTTACAGAGAGAGAACTGGGCTGGCAGAA 418
DB 1611 CAGGTCTAGTGTCTTAACCTTGGAGAAAGTATGTAGCAGCTTAACGAGCAATGTGTAA 1670
QY 419 CCAGAGCTAGCCCAAGATTACCAAGT 445
DB 1671 TTGTTCAACTTGAACACTACGAGGT 1697

RESULT 15
BO778458 606 bp mRNA linear EST 26-JUL-2002
LOCUS Homo sapiens, clone IMAGE:6031548 3,
DEFINITION mRNA sequence.
ACCESSION BO778458
VERSION BO778458.1 GI:21986930
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 606)
AUTHORS Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritzer, E., Rojko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, R., Williams, T., Jackson, Y., and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: 1131d07.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium

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MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 450.

FEATURES

SOURCE

1..606

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAG:6031548"

/tissue_type="Purified pancreatic islet"

/lab_host="DH10B"

/clone_id="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match

6.5%; Score 197.8; DB 13; Length 606;

Best Local Similarity 78.2%; Pred. No. 2.3e-14;

Matches 251; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

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QY 20 GCCGGGCGGGTGGCTCAAGCCTGTAATCCAGACATTGGAGGTCGAGCGGGTGGAC 79
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Db 191 GCCAGGACGCTGGCTCAGCCTGTAATCCAGACATTGGAGGTCGAGCGGGTGGAT 250
QY 80 CACCTGGGGTCAGAGATTGAGACCAAGCTGGCCACATGGCGAAACCTGACTACACAA 139
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Db 251 CACCTGAGGTCAGAGATTGAGACCAAGCTGGCCACATGGCGAAACCTGCTCTACTA 310
QY 140 AAAACACAAAATTAGCCGGG---GCTTGGGCGCTCCTGTCGTCGCCAGCTACTCAGGAG 196
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Db 311 AAAGTACAAAATTAGCTGGGTGTGTGTGGCGGGTGCCTGTCTATCCAGCTACTCAGGAG 370
QY 197 CTGAGGTGGAGGAGCTGCTTGAAGCTGGAGAGTCGAGGCTGACGTGATTCGGCG 256
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QY 257 CACTTAACCTCAGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 316
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Db 431 CACTGCACTCAGCCTGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 490
QY 317 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 337
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Search completed: July 17, 2004, 23:34:04
Job time : 7454 secs

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